

1 31  
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC  
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91  
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC  
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

# Cadherin

121 151 |xx EC motif xx|  
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC  
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211  
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC  
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271  
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA  
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331  
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT  
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391  
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA  
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451  
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG  
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481 511  
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG  
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571  
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC  
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631  
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA  
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661

CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT  
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

691

721

ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT  
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

751

781

GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA  
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro

811

841

GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG  
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

871

901

AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT  
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

931

961

ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT  
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

991

1021

CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC  
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn

1051

1081

TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC  
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1111

1141

AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA  
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1171

1201

GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT  
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1231

1261

TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA  
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1291

1321

GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG  
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1351

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1381
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441
CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501
GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561
GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621
|xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxx
AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx|

1711
TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

1741
AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

1801
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1861
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041
|xxxxx ITAM xxxx|
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

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2101 2131  
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG  
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2161 2191  
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT  
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2221 2251  
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC  
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2281 2311  
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC  
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2341 2371  
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT  
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2401 2431  
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC  
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2461 2491 |xxxxxxxxxxxxxxxxxxxxxxxxxxxx  
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA  
arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

xx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA  
asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

xx| 2611  
AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG  
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641 2671  
GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC  
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701 2731 |xxxxxxxxxxxx  
AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA  
asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

xx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx  
AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT  
asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

XX|

AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG  
asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881 2911  
CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA  
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941 2971  
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG  
cys glu thr gln leu ser gln gly ser OCH glu lys pro ser ser phe val glu thr val

3001 3031  
GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG  
ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln

3061 3091  
GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA  
asp STP

3121 3151  
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181 3211  
GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241 3271  
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301 3331  
TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361 3391  
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421 3451  
TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

3481 3511  
AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

3541 3571  
ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA

3601 3631  
CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG

3661 3691  
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG



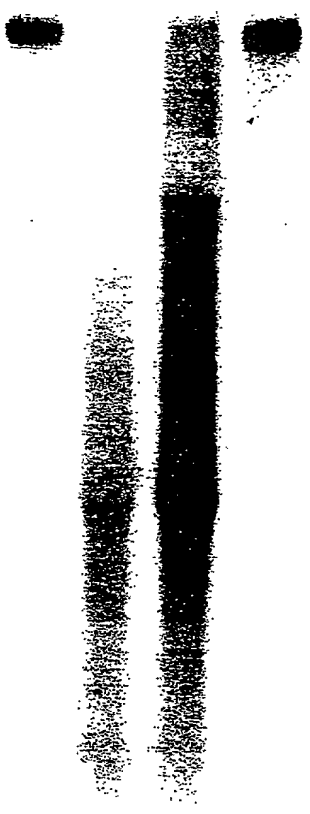
54 kb

A

FIG. 2

~ 7.5 kb —

Jurkat  
MV4-11  
THP  
HL60  
9D10  
CH27  
3A9  
293



**B**

FIG. 2



00936650-124300

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSAES
HC5	-----



00736650-134300

HC2A KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS  
 KIAA KDLLGAISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS  
 rat -----  
 HC4 TDKDTAYGSFQNG-----HGIKREDSRGS LIP-EGATGFDPQNGTGEN-----TRQS  
 HC1 KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL  
 HC3 QTVAMAIAGTSPVQ-----LTRPGSFLLTSTSGRQHT-----  
 HC5 QNVALAIAGNFN-----LKTSG-IVLSSLPYKQYN-----

HC2A TLGNSVVRCDKLDQSEIKSLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL  
 KIAA TLGNSVVRCDKLDQSEIKSLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL  
 rat -----  
 HC4 STRSSVSQYNRLDQYEIRSLMICYLYIVKMISED TLLTYWN-KVSPQELINILILLEVCL  
 HC1 ALIGSTLRFDRLDQAETRSLMCF LHMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL  
 HC3 -----TFSAESSRSLICLLWLKN-ADETVLQKWF TDL SVLQNLRLDLLYLVCV  
 HC5 -----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFQYMGKRYIARNQEG LG--PIVHDRKS-----QTLPVSRNRTGMM  
 KIAA HQFQYMGKRYIAR-----TGMM  
 rat -----  
 HC4 FHFRYMGRNIARVHDAWLSKHFGIDRS-----QTMPALRNRSQVM  
 HC1 QNFRYL GKRNIIIRKIAAAF--KFVQSTQNNGT LKGSNPSCQTSGLLAQWMHSTSRHEG HK  
 HC3 SCFEYK GKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV  
 HC5 LCFEYK GKQSSDKVSTQVLQ--KSRDV KAR-----LEEALLRGEGARGEMM

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC  
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC  
 rat -----  
 HC4 QARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS  
 HC1 QHRSQTLPIIRGK---NALS NP KL---LQMLDNTMTS NSNEIDIVHHVDTEANIATEGC  
 HC3 RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNT EKLDKSRAEIEHEALIDGNLATEAN  
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAE LDQEALISGNLATEAH

HC2A LTALDTLSLFTLAFKNQLLADHGHNP LMKKVFDVYLCFLQKHQSE TALKNVFTALRSLIY  
 KIAA LTALDTLSLFTLAFKNQLLADHGHNP LMKKVFDVYLCFLQKHQSE TALKNVFTALRSLIY  
 rat -----KLSRGHSP LMKKVFDVYLCFLQKHQSE MALKNVFTALRSLIY  
 HC4 LTVLDTISFFTQC FKT HFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS  
 HC1 LTILDVLSLFTQTHQRQLQCCDCQNSLMKRGFD T YMLFFQVNO SATALKHVFASLRLFVC  
 HC3 LIILD TLEIVVQTVS--VTES--KESILGGVLKVLLHSMACNQSAVYLQHC FATQRALVS  
 HC5 LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNC DQSTTYLTHCFATLRALIA

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRN NFDYT GKKS FVRTH  
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRN NFDYT GKKS FVRTH  
 rat KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRN NFDYT GKKS FVRTH  
 HC4 KFPSAFFKGRVNMCAAF CYEVLKCCTSKISS TRNEASALLYLLMRN NFEYTKRKTFLRTH  
 HC1 KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH  
 HC3 KFPELLFEEETEQCADLCRLRLRHCS SIGTIRSHPSASLYLLMRQNFEIGN--NFARVK  
 HC5 KFGDLLFEEVEQCFDLCHQVLHHCSSMDVTRSQCATLYLLMRFSFGATS--NFARVK

HC2A LQVIIISVSQLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM  
 KIAA LQVIIISVSQLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM  
 rat LQVIIISLSQLIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM  
 HC4 LQIIIAVSQLIADVALSGGSRFQESLFI INNFANS DRPMLARAFPAEVKDLTKRIRTVLM  
 HC1 LQLIKAVSQLIAD-AGIGGSRFQHSLAITNNFANGDKQMKNSNFP AEVKDLTKRIRTVLM  
 HC3 MQVPMSLSSLVGTSQNFNEEFLRRSLK TILTYAEEDLELRETTFPDQVQDLVFNLMILS  
 HC5 MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQMT PFPTQVEELL CNLNSILY

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL	LSEAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL	LSEAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGL	LSEAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKTWLD SMAKIHVKNGL	FSEAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLES MAKIHARNGI	LSEAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTS PDLRLTWLQNMAGKHSERSN	HAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQAS PDLRLTWLQNMAEKHTKKKQ	YTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYI	TRKGV-----	FRQGCTAFRVITPN
KIAA	TALVAEYI	TRKEA-----	VQWEPPLLPHSHSACLRRSRGGVFRQGCTAFRVITPN
rat	TALVAEYI	TRKEAD-----	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRVITPN
HC4	AALVAEFI	HRKKL-----	FPNGCSAFKKITPN
HC1	AALIAEYI	KRKGWYKVEKIC	TASLLSEDPHPCDSNSLLTTPSGGSMFSMGWPAFLSITPN
HC3	AALVAEYI	SMLED-----	RKYLPGVCVTFQNISSN
HC5	AALVAEYI	SMLED-----	HSYLPVGSVVSFQNISSN

ITAM

HC2A	I DEEASMMEDVGMQD-----	VHFNEVDLMELLEQCADGLWKAER	YELIADIYKLI	IPI
KIAA	I DEEASMMEDVGMQD-----	VHFNEVDLMELLEQCADGLWKAER	YELIADIYKLI	IPI
rat	I DEEASMMEDVGMQD-----	VHFNEVDLMELLEQCADGLWKAER	LRAGLLTSINSSSP	
HC4	I DEEGAMKEDAGMMD-----	VHYSEEVLLELLEQCNGLWKAER	YETI	ISEISKLIGPI
HC1	IKEEGAAKEDSGMHD-----	TPYNENILVEQLYMCGEFLWKSER	YELI	ADVNPPIIAV
HC3	VLEESAVSDDVVSPEEGICSGKYFTESGLVGLLEQAAAS	FSMAGMYEAVNEVYKVL	IPI	
HC5	VLEESVVSSEDTLSPDEGVCAGQYFTESGLVGLLEQAAEL	FSTGGLYETVNEVYKVL	IPI	

	ITAM	ITAM	ITAM	ITAM						
HC2A	YEKRRD-----									
KIAA	YEKRRD	FERLAHL	YDTI	HRAYS	SKV	TEVMHSGRLL	LGTY	FRVA	FFGQAAQYQ	FTDSETDVE
rat	SMKSGGT	LETTHLY	DTI	HRAYS	SKV	TEVITR-----	A-----	AGSWDLL	PGGLFGQ	
HC4	YENRREF	ENLTQVY	RTI	HGAY	TKILEVM	HTKKRL	LG-----	TFFRV	AFYFGQ	
HC1	FEKQR	DFKKLS	DL	YDY	HRSYL	KVAE	VVNSEK	RLFG-----	RYRVA	AFYFGQ
HC3	HEANR	DAKKL	STI	HGKL	QEA	FSKIV	HQSTG	WERMFG-----	TYFRV	GFYFG-
HC5	LEAHRE	FRKLT	LT	THSKL	QRA	FDSIV	NKDH--	KRMFG-----	TYFRV	GFYFG-

	ITAM	ITAM			
HC2A	-FFEDEDG	KYIYKEPKLTPLSEISQRL	KIYSDKFGSENVKMIQDSGKVNPKDLDSK	YA	
KIAA	GFFEDEDG	KYIYKEPKLTPLSEISQRL	KIYSDKFGSENVKMIQDSGKVNPKDLDSK	YA	
rat	GFFEDEDG	KYIYKEPKLTPLSEISQRL	KIYSDKFGSENVKMIQDSGKVNPKDLDSK	FYA	
HC4	SFFEDEDG	KYIYKEPKLTGLSEISLRL	VKIYGEKFGTENVKIIQSDKVNAKELDP	KYA	
HC1	GFFEEEEG	KYIYKEPKLTGLSEISQRL	KIYADKFGADNVKIIQDSNKNVNPKDLDP	KYA	
HC3	TKFGDL	DEQEFVYKEPAITKLAE	ISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDP	NKA	
HC5	SKFGDL	DEQEFVYKEPAITKLPE	ISHRLEAFYGC	FGAEFVEVIKDSNPVDKCKLDP	NKA

ITAM

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA	
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA	
rat	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVVEEQCKRRTILTA	
HC4	HIQVTVYKPYFDDKELTERKTEFERHNISRFVFEAPYTLSGKKQGCIEEQCKRRTILT	
HC1	YIQVTVYVTPPFEEKEIEDRKTD	FEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILT
HC3	YIQITTYVEPYFDTYEMKDRITYFDKNYNLR	RFMYCTPFTLDGRAHGEHQFKRKILT
HC5	YIQITTFVEPYFDEYEMKDRVITYFEKNFNL	RRFMYTTPFTLEGRPRGELHEQYRRNTVLT

Coiled-Coil 1

HC2A	IHC	FPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQSV
KIAA	IHC	FPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQSV
rat	IHC	FPYVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQSV
HC4	SNS	FPYVKKRIPIN	CEQQINLKE	IDGATDEIKDKTAELQKLCSTDVDMIQQLKLQWV
HC1	SHL	FPYVKKRIQV	ISQSSTELN	IEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQSV
HC3	SHAF	PIKTRVNVTH	KEEIILTF	IEVAIEDMQKKTQELAFATHQDPADPKMLQMVLOQSV
HC5	MHAF	PIKTRISVIQ	KEEFVLTF	IEVAIEDMKKKTLQAVAINQEPPDAKMLQMVLOQSV

Coiled-Coil 2

HC2A	SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLDDTNTKRYPDNKVKLLKEVFRQFVEACGQALAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLNDSQASKYPKKVSELKDMFRKFIQACSI ALELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQALDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKKNKSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEAVEKNKRLITADQRE

Coiled-Coil 2

HC2A	YQEEMKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTPPTSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHE	QLG-----
rat	YQEEMKANYREIRKELSDIIVERICPGEDKRATKFPAPHLQRHQRDTNKHSGSRVDQFILS	
HC4	YHEGLKSNFRDMVKELSDIIEHQILQEDTMHSPWMSNTLHVFCASISGTSSTRGYGSPRYA	
HC1	YQEELRSHYKDMSELSTVMNEQITGRDDLK---	RGVDQTCRTRVISKATPALPTVSISS
HC3	YQRELG----	KLSS-----PZ-----
HC5	YQQLKKNYNKLKENLRPMIERKIPELYKPIFRVESQKRDSFHRSSFRCKETQLSQGSZ-	

PBM

HC2A	SSVVZ-----
KIAA	-----
rat	CVTLPEPHVGTCTVMCKLRTTFRANHWFCQAQEEAMGNGREKEPWTVIFNSRFYRSWGK
HC4	EVZ-----
HC1	SAEVZ-----
HC3	-----
HC5	-----

HC2A	----
KIAA	----
rat	VHIFF
HC4	----
HC1	----
HC3	----
HC5	----

[illegible]

D

E

	F	G	
CLASP-1	SEQLKLQGSVSVQVNAGPMAYARAFLEETNAKKYPDNQV--KILKEIFRQFADACGQALD		
TRG	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYPDONKV--KILKEVFRQFVEACGQALA		
KIAA1058	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYPDONKV--KILKEVFRQFVEACGQALA		
CLASP-2	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYPDONKV--KILKEVFRQFVEACGQALA		
CLASP-6	KLQLKLQGSVSVQVNAGPLAYARAFLLDDTNTKRYPDONKV--KILKEVFRQFVEACGQALA		
CLASP-3	MLQMVLLQGSVGTTVNQGLEVAQVFLSE--IPSDPKLFRHHNKLRLCFKDFTKRCEDALR		
CLASP-4	QLQLKLQGCVSQVNAGPLAYARAFLLDSQASKYPPKKVSELKDMFRKFI--QACSIALL		
CLASP-5	MLQMVLLQGSVGATVNQGLEVAQVFLAE--IPADPKLYRHHNKLRLCFKEFIMRCGEAVE		
KIAA0716	PLTMCLNGVIDAAVNGGVSRYQEAFVKEYILSHPEEDGEKIARLRRLMLEQAQILEFGLA		
DOCK2	PLSMLLNGIVDPAVMGGFAKYEKAFFTEEYVRDHPEDQDKLTHLKDLIAWQIPFLGAGIK		
DOCK3	LLSMCLNGVIDAAVNGGIARYQEAFDKEYINKHPGDAEKITQLKELMQEQVHVLGVGLA		
DOCK180	PLSMLLNGIVDPAVMGGFAKYEKAFFTEEYVRDHPFAHEKIEKLKDLIAWQIPFLAEGIR		
CONSENSUS	L M L+G V VN G Y AFL + + P L+ L		
	L I V V F + I		

DOCK1=KIAA0289  
DOCK3=KIAA0299  
CLASP variant=KIAA1058

ref 1.1 ↓

1 31  
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC  
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91  
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC  
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 151  
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC  
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211  
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC  
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271  
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA  
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331  
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT  
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391  
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA  
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451  
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG  
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481 511  
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG  
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571  
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC  
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631  
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA  
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661 691  
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT  
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721 751  
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT  
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781 811  
GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA  
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro



841 871  
GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG  
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901 931  
AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT  
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

961 991  
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT  
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021 1051  
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC  
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn  
↓ ref 3.1

1081 1111  
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC  
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141 1171  
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA  
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201 1231  
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT  
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261 1291  
TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA  
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321 1351  
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG  
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381 1411  
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT  
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441 1471  
CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA  
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501 1531  
GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT  
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561 1591  
GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG  
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621 1651  
AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG  
lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

1681	1711
TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG	GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu	asp his ser tyr leu pro val gly ser val
1741	1771
AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG	GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu	glu glu ser val val ser glu asp thr leu
1801	1831
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC	CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly	gln tyr phe thr glu ser gly leu val gly
1861	1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC	ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser	thr gly gly leu tyr glu thr val asn glu
1921	1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA	GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu	ala his arg glu phe arg lys leu thr leu
1981	2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC	AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp	ser ile val asn lys asp his lys arg met
2041	2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT	GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe	gly ser lys phe gly asp leu asp glu gln
2101	2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC	AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr	lys leu pro glu ile ser his arg leu glu
2161	2191
CGCA TTT TAT GGT CAA TGT TTT GGT GCA GAA	TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu	phe val glu val ile lys asp ser thr pro
	ref 4.1
2221	2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG	GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys	ala tyr ile gln ile thr phe val glu pro
2281	2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG	GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg	val thr tyr phe glu lys asn phe asn leu
2341	2371
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC	CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr	leu glu gly arg pro arg gly glu leu his
2401	2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC	ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr	thr met his ala phe pro tyr ile lys thr
2461	2491
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT	GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe	val leu thr pro ile glu val ala ile glu

2521	2551
GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA	GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu gln leu ala	val ala ile asn gln glu pro pro asp ala
2581	2611
AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT	GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
lys met leu gln met val leu gln gly ser	val gly ala thr val asn gln gly pro leu
2641	2671
GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT	CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile	pro ala asp pro lys leu tyr arg his his
2701	2731
AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC	ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
asn lys leu arg leu cys phe lys glu phe	ile met arg cys gly glu ala val glu lys
2761	2791
AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG	GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
asn lys arg leu ile thr ala asp gln arg	glu tyr gln gln glu leu lys lys asn tyr
2821	2851
AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG	ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
asn lys leu lys glu asn leu arg pro met	ile glu arg lys ile pro glu leu tyr lys
2881	2911
CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG	GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg	asp ser phe his arg ser ser phe arg lys
2941	2971
TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA	GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH	
↓ ref 5.1	
3001	3031
GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG	TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG
3061	3091
GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC	ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA
3121	3151
TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG	ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG
3181	3211
GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT	TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC
3241	3271
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA	CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA
3301	3331
TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG	AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA
3361	3391
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA	TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC
3421	3451
TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT	CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA
3481	3511

AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

3541 3571  
ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA

3601 3631  
CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG

3661 3691  
CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG

3721 3751  
CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA

3781 3811  
AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT

3841 3871  
CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT

3901 3931  
TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT

3961 3991  
GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA

4021  
AAC TCG

## References

BAC sequences of Human CLASP 5

### Ref 1.1

Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA. Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCCAGGTTATAAAGNATTATTTACTAAAAGAANATTCANGC  
TATTTTCATTTAACTAGCTCAGTTTAATCATGTATTTTCTATAAAGGTTAGTCTTATTAAT  
TTGACAAAACAATCAAACAATTCAAACCAGATCAAGTATGCTACCCTGAAGTTACACC  
ACTAGCTAAGAATTAACAATCTAAGTAATTGGTTTCTCCCCAGGCTCAAGGCTCCCTGA  
TCAGGTTAAGTAAAGCCAAGAATCCAATAAGCCCTATGAAATTTAGAACTCATAGAA  
AAGTCTCAAATCTTCTTGTCTGACATTAGCCAATTGTTATATTATGCAAATAGAGGATT  
NCAAGTAAATAAGTTTGGAACCTGTTTACCAGGTTTTTGCAGCAGNCCTCTAAGAGCTT  
AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNGG  
TTCCAATNTTACTGGAACCCACCACTATCTTTNGAAGTCTTGATACTTAACTGNGTGTA  
GNCTCTTTAGGCCTNTANTAANTAGAATCTATATGGATTTCGTGTTCTGTCNGCAAGNAG  
TGCCTATGAAA

### Ref 2.1

Sequence of BAC19 using primer HC5AS10b, which spans nucleotides 560-580 of the cDNA.

Exon sequence is underlined and represents nucleotides 510-553.

TGCGAGTAGTGTCCGCGTTCAGCATGTTGTACTGCTTATAGGGCTGAAGGGAGGCACG  
ATTGGGGGATGGAGGCCAGGGAAGAAGTCAAGCAACAGAAAAATTTGAGGCTTAACA  
GTCAAGCAACAGAAAAATTCAAAGTGTTCTCTTAAAATACCATGACTGTACATCACTG  
CTAGGCTGGAGATCTATTGCCAGTAGCCCTGCCTTCCCTAGGCAGGGGAAGCTGTGTT  
CTTTGAGTAGCGCTACTCAGCAAAGAGGCTCACCTGGGGCAGTATTTGAGCTAGGCTT  
TCAGCCACCGTATCTGAGTACCTCTGTCTTANGAGCAGTGTGGCCTGGTGATCACCCCT  
GGGCCTTGATCATGCGTGCTGCAATCCCAGTGATACAAAGAGGCTTTCATGCTGCTAA  
GATCTCCAAGTATTTCTCCTTCGTGCTGGGCAGCAGAGGGTTAGACTTNCAGGGGAGA  
AGGAACTGGCTGGGTGCCATGAATAANCTTGCTGTTCAAGANTTAACCTTCTTTGTTAC  
ATAAGNGCAAAGGTATAACATAAAGGGNCATGAACTGCTCAACNAAATTNATCAAAT  
CCATGTTTGTGGGAGTTCCTTTGTNATNGGAAGTTTAACCCCTAA

### Ref 3.1

Sequence of BAC13 using primer C5S3, which spans nucleotides 1086-1105 of the cDNA. Exon sequence is underlined and represents nucleotides 1110-1120.

CCNGCTCTTTTTGGCAANGTAANCTTGGGATGCTTGTTTTCTTCCTCTTAATTAAGAG  
NAAGANTTTTTTTAGCTTCATACTTCTCTCTTCAGGGGGACCAAAAGTCACAGAGCATA  
TTAAGTGGCANAAACCCNAAGGTCTTAAGTCTTCCTAGGAAGAAAGCAGATGCCCTGA  
TTCTGTGGGAAGCCACCATGGAGAGGAAAAGCAGTGGCTCCCATATTTGAAGTGNGGA  
CCTAACTCTAGAAAGTTTAAAANGGCCATTTGCTGAAGGGCTATGACATGAGAACAGA  
GATCAACTGAGTGACTTAGCAANTTCACTCTTTCTCTGTAANACCTCTGGTGAGTGAGA  
NTAAATCCTNTATGTGACGCCCATTAGTCTTACAAAANGTCATGCCNTAAAATGCCAN  
GAAGGNCAGAAATGAATTTCTCACCGCCNGAGGAATGAGGATTATNCTGGGGGGACA  
TGCANAAATATTNNNCCCCCNATTTATTNATTTATTTATTTTTGAGACNGAGTNTCGNT  
CTAATCGCCCCCAGGCTGGNAGGTGGNAGGTGGTTCCCATCTTNAANCTTANNTNGGA  
AGGNCCTCTTTGNGCCCCNGGGGGGNGNAAAGNGAATTCCCTAAATGCCTNCANNCCC  
CTCCCTGGANGTTATTTGGGGGNNTTNTAAAGGGCNGTGCCNG

### Ref 4.1

Sequence of BAC13 using primer C5S7, which spans nucleotides 2196-2205 of the cDNA. . Exon sequence is underlined and represents nucleotides 2225-2231.

ACAAAACTAACCATCANTCTCTAAATCCCAACAANCTTTTTTTAAGAATACCTAANG  
AGCTCAACNAGGGGGACTNTCCAANGCACTTAAATGCAGNCAAACNACNCCNNCAAG  
AGNGGCAACTACTAATGGGGCANATCTNAAAGAAAATATAGNCAAAGGNNGGAATCA  
TAATAGGAGCNACCACTTANGAAGCACCAACTGGGGACCTGGAAGTGNATNAGGNCC  
TCTACATACATCATNNNATANCATCCTGCAACGACCCCTGGAAGGAGANAGANGGNA

TTCCTANNNTAGAGANGAGANAACCTGGGGACATGGGAAGAGGNAAGCGAAGGGTTCA  
AGGGGANGNAAGCGAGCAGANNCCAGGGNCTCANACTNGNGGGGNNTGGGGGGNTN  
CTGNNNCCCTACNCTTNGNANGAACAGNGNNGTTGANNTGGCTTTNGANTA

#### Ref 5.1

Sequence of BAC13 using primer 122047F1, which spans nucleotides 3537-3556 of the cDNA.

Exon sequence is underlined and represents nucleotides 3000-3492. This region does not contain a  
intron in this region

CCANNAGATTNTTGNAACGNNGGTAGGCTTCCTTTGTAGATTTATTGAAAATGTTTCGT  
ACTTCTACAAGTTTGCCCTGCCTTCCTATAAAGAGTGAAANTCANTTTGAATCGACTGG  
TGGATAATTNTTCCATTTTTCTCAGGCAATTTNGAGTTACTCCAATAAATTCAAATAT  
GGGCCAGAGGAAATCATCTTTCAGATGGGCAGTGATTGGCCAGTCAGCAGGAGAAGC  
TGCTTATGCCTTGTTTGGTACATTGTGGAAAAACACACTTTAATAAATACGCANTCATG  
CCTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT  
CCATTTGGGAATAATTCCATGGTTCCTGGGATCCCAAAGCTTCCAGAAGTGCTGGCTG  
ATCAANGGAGTGTACAGTCAGTCCTGGGTGGCAAAAATGTCCCATTTTTTAAGTACCA  
AGCAAAGGTTCTTCTTCAAGGGTTNCTAGGGCC

0066767-0565E

Figure

Multiple sequence alignment of Human CLASP proteins with intron/exon borders indicated by a vertical line. Numbers in right margin correspond to References

```

HC2A -----
KIAA  ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat   -----
HC4   -----
HC1   -----
HC3   -----
HC5   -----

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```

HC2A -----
KIAA  FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat   -----
HC4   -----
HC1   -----
HC3   -----
HC5   -----

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```

HC2A -----VLHHHQNPEFYDEIK
KIAA  KSAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPEFYDEIK
rat   -----
HC4   -----
HC1   -----
HC3   -----
HC5   -----

```

```

HC2A  IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA  IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat   -----
HC4   -----
HC1   -----
HC3   -----
HC5   -----

```

```

HC2A  PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
KIAA  PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
rat   -----
HC4   -----
HC1   -----
HC3   -----GPGPARSTVSIISLISNSARV
HC5   -----

```

```

HC2A  QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA  QKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat   -----
HC4   -----MEIQVLIRFLSVILMQLFVLPNMIHEDDVPISCPMV
HC1   -----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3   NRSRSLSNSNPDISGTPSPDDEVRSIIGSKGLDRSNSWNTGGPKAAPWGSNPSPSAES
HC5   -----

```

B

HC2A I IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN  
 KIAA I IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN  
 rat -----  
 HC4 LFHIVSKCHEEGLDLSYSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN  
 HC1 LPDIVAKCHEEQLDHSVQSYIKFVKTR---ACKERPVEDLAKNVTGLLK-SNDSPTVK  
 HC3 TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSSG--SVF---E  
 HC5 -----

## Cadherin

## Cleavage

HC2A KLLRYSWFFFDVLIKSMAQHLENSKVKLIRNORFPASYHHAAETVVNMLMPHITQKFGD  
 KIAA KLLKYSWFFFDVLIKSMAQHLENSKVKLIRNORFPASYHHAVETVVNMLMPHITQKFRD  
 rat -----  
 HC4 KLLKYSWFFFEIIAKSMATYLLEENKIKLTHGQRFPPKAYHHALHSLFLAIT-IVESQYAE  
 HC1 HVLKHSWFFFAIILKSMAQHLEIDTNKIQLERPQRFPPESYQNELDNLMVLSDHVIWKYKD  
 HC3 SALQQAFFFEFLVKSVMVHLLYFNDKLEAPRKSRFPERFMDIAALVSTIASDIVSRFQK  
 HC5 -----

HC2A NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDEKTLFEYKFEFL  
 KIAA NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL  
 rat -----  
 HC4 IPKESRNVNYSLASFLKCCLTLMDRGFVFENLIN---DYIS--GFSPKDPKVLAEYKFEFL  
 HC1 ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQYKFDLFL  
 HC3 DTEMVERLNTSLAFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPVSIVSLRDLFL  
 HC5 -----

HC2A RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF  
 KIAA RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF  
 rat -----  
 HC4 QTICNHEHYIPLNLPM-----AFAPKPKLQR-----YQDSNL----EYSLSTEY  
 HC1 QEVCQCHEHFIPCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF  
 HC3 RIICSHEHYVTNLNPLCSLLTPPASPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF  
 HC5 -----MNADTAPTSPCPSIS--SQSSSCSSSQDQKIASMFDRTSRVPA 1.1

## Cadherin

## EC motif

HC2A CRNHFLVGILLREVGITALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 KIAA CRNHFLVGILLREVGITALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT  
 rat -----  
 HC4 CKHHFLVGILLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ  
 HC1 CRKHFLIGILLREVGIFALQEDQD----VRHLALAVLKNLMKHSFDDRYREPRKQAQIAS  
 HC3 RQQHYLAGIVLTELAVILDPAEGLFGLHKKVINMVHNLSSHDSDPYSDPQIKARVAM  
 HC5 SSTS-SPGILLFTELAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPKVCVPEVKVIAA

HC2A LYLPLFGLLIENVRINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH  
 KIAA LYLPLFGLLIENVRINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH  
 rat -----  
 HC4 LYLPLFVGLLLENIQRLAGRDITLYSCAMPNSASRDEFPCG-----FTSP--AN--RGSLS  
 HC1 LYMPLYGMLLDNMPRIYLDLYPFTVNTSNQGSRDDLTNGGFQSQTAIKHANSVDTSFS  
 HC3 LYLPLIGIIMETVPQLYDFTETHNQGRPICIAATDDYESE-----SG---SMIS  
 HC5 LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT



HC2A KLLGAIISGIAEPTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS lets  
 KIAA KLLGAIISGIIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS  
 rat -----  
 HC4 TOKDTAYGSFONG-----HGIKREDSRGSLIP-EGATGFPDQNGTGEN-----TRQS  
 HC1 KDVLSNIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL  
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----  
 HC5 CNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN----- 2.1

HC2A TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL  
 KIAA TLGNSVVRCDKLDQSEIKSLLMCFLYILKSMSDDALFTYWN-KASTSELMDFFTISEVCL  
 rat -----  
 HC4 STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLTYWN-KVSPQELINILILLEVCL  
 HC1 ALIGSTLRFDRLDQAEIRSLLMCFLHIMKTISYETLIAYWQ-RAPSPEVSDFFSIIIDVCL  
 HC3 -----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLLYLCV  
 HC5 -----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRLDLLFICV

HC2A HQFYMGKRYIARNQEGLG--PIVHDRKS-----QTLFVSRNRTGMM  
 KIAA HQFYMGKRYIAR-----TGMM  
 rat -----  
 HC4 FHFRYMGRNIARVHDANLSKHFGIDRKS-----QTMPALNRNSGVM  
 HC1 QNFRYLGRNIIRKIAAAF--KFVQSTONMGTILKGSNPSCQTSGLLAQNMHSTSRHEGKH  
 HC3 SCFEYKGGKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV  
 HC5 LCFEYKGGKQSSDKVSTQVLQ--KSRDVKA-----LEEALLRGEGERGEMV

HC2A HARLQQL-----SSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC  
 KIAA HARLQQL-----SSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC  
 rat -----  
 HC4 HARLQHL-----SSLESS-----FTLNHSSTTTEADIFHQALLEGNTATEVS  
 HC1 HRSQTLPIIRGK---NALSNPKL---LQMLDNTMTNSNEIDIVHHVDTEANITEGC  
 HC3 PRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN  
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQREALISGNLATEAH

HC2A LTALDTLSLFTLAFINQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY  
 KIAA LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRSLIY  
 rat -----  
 HC4 LTVLDTISFFTQCFKTHFLNNGHNPMLKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS  
 HC1 LTILDVLSLFTQTHQRCLQQCDQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVC  
 HC3 LTILDTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLQHCFAQRALVS  
 HC5 LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDDQSTTYLTHCFALRALIA 3.1

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH  
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH  
 rat -----  
 HC4 KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH  
 HC1 KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH  
 HC3 KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH  
 HC5 KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTH

HC2A LQVIIISVSQLIADVVGIGETRFOQSLSIINNANSRDRIKHTSFSSDVKDLTRIRTVLM  
 KIAA LQVIIISVSQLIADVVGIGETRFOQSLSIINNANSRDRIKHTSFSSDVKDLTRIRTVLM  
 rat -----  
 HC4 LQVIIISVSQLIADVVGIGETRFOQSLSIINNANSRDRIKHTSFSSDVKDLTRIRTVLM  
 HC1 LQVIIISVSQLIADVVGIGETRFOQSLSIINNANSRDRIKHTSFSSDVKDLTRIRTVLM  
 HC3 LQVIIISVSQLIADVVGIGETRFOQSLSIINNANSRDRIKHTSFSSDVKDLTRIRTVLM  
 HC5 LQVIIISVSQLIADVVGIGETRFOQSLSIINNANSRDRIKHTSFSSDVKDLTRIRTVLM



~ 11 kb →

~ 5.7 kb →

~ 5.0 kb →

HindIII

Eco RI

Genomic DNA

HindIII

Eco RI

→

→

→

> 14 kb

~ 13 kb

~ 4.4 kb

BAC #19 DNA

**Table 1**

-111

CGGTAACCGCCATTTTGTCTCCTGTAACAATTTACGCGCCGTGTAAGTCTTTCAAAGCCTCAGTTTTATGACC  
CTGTGGAGCCAGTGGACTTTGAAGGACTTCTG -1

1/1 31/11  
ATG ACA CAC CTG AAC AGC CTG GAT GTG CAG CTT GCC CAG GAG CTC GGG GAC TTC ACT GAT  
Met thr his leu asn ser leu asp val gln leu ala gln glu leu gly asp phe thr asp  
61/21 91/31  
GAC GAC TTG GAC GTG GTG TTC ACG CCA AAG GAA TGT AGG ACT TTG CAG CCC TCT TTG CCG  
asp asp leu asp val val phe thr pro lys glu cys arg thr leu gln pro ser leu pro  
121/41 151/51  
GAG GAA GGG GTT GAA CTG GAC CCT CAT GTC AGG GAC TGT GTT CAG ACC TAC ATC CGT GAG  
glu glu gly val glu leu asp pro his val arg asp cys val gln thr tyr ile arg glu  
181/61 211/71  
TGG CTA ATC GTG AAC CGG AAA AAC CAA GGA AGT CCA GAA ATC TGT GGC TTT AAA AAG ACT  
trp leu ile val asn arg lys asn gln gly ser pro glu ile cys gly phe lys lys thr  
241/81 271/91  
GGA TCT CGA AAA GAT TTT CAC AAG ACG CTT CCG AAA CAG ACG TTT GAG TCG GAA ACC TTG  
gly ser arg lys asp phe his lys thr leu pro lys gln thr phe glu ser glu thr leu  
301/101 331/111  
GAG TGC AGT GAA CCC GCT GCT CAG GCA GGC CCC CGC CAC TTA AAC GTG CTG TGC GAC GTG  
glu cys ser glu pro ala ala gln ala gly pro arg his leu asn val leu cys asp val  
361/121 391/131  
TCT GGG AAA GGC CCC GTC ACT GCC TGT GAC TTT GAC CTC CGC AGC CTG CAG CCT GAC AAG  
ser gly lys gly pro val thr ala cys asp phe asp leu arg ser leu gln pro asp lys  
421/141 451/151  
CGG CTA GAA AAC CTC CTG CAG CAA GTG AGT GCC GAG GAC TTT GAG AAG CAG AAC GAG GAG  
arg leu glu asn leu leu gln gln val ser ala glu asp phe glu lys gln asn glu glu  
481/161 511/171  
GCC CGG AGG ACC AAC AGG CAG GCC GAG CTC TTT GCC CTT TAC CCA TCA GTG GAC GAG GAG  
ala arg arg thr asn arg gln ala glu leu phe ala leu tyr pro ser val asp glu glu  
541/181 571/191  
GAT GCT GTG GAA ATA CGT CCA GTA CCA GAA TGT CCC AAG GAA CAC CTG GGC AAC AGA ATA  
asp ala val glu ile arg pro val pro glu cys pro lys glu his leu gly asn arg ile  
601/201 631/211  
TTG GTC AAG TTG CTG ACC TTG AAG TTC GAG ATT GAA ATT GAG CCC CTG TTT GCC AGC ATT  
leu val lys leu leu thr leu lys phe glu ile glu ile glu pro leu phe ala ser ile  
661/221 691/231  
GCC CTC TAC GAT GTT AAA GAA AGG AAA AAG ATC TCA GAA AAT TTT CAC TGT GAC CTG AAC  
ala leu tyr asp val lys glu arg lys lys ile ser glu asn phe his cys asp leu asn  
721/241 751/251  
TCT GAC CAG TTC AAA GGA TTT CTG CGA GCT CAC ACG CCT TCA GTG GCC GCA TCA AGT CAG  
ser asp gln phe lys gly phe leu arg ala his thr pro ser val ala ala ser ser gln  
781/261 811/271  
GCG AGA TCT GCA GTC TTC TCA GTC ACC TAC CCG TCC TCA GAC ATC TAC CTG GTA GTC AAG  
ala arg ser ala val phe ser val thr tyr pro ser ser asp ile tyr leu val val lys  
841/281 871/291  
ATT GAA AAA GTC CTG CAG CAG GGA GAT ATT GGA GAC TGT GCA GAG CCC TAC ACG GTT ATC  
ile glu lys val leu gln gln gly asp ile gly asp cys ala glu pro tyr thr val ile  
901/301 931/311  
AAA GAA AGT GAT GGT GGA AAG AGT AAA GAA AAG ATT GAA AAA CTA AAA CTC CAA GCT GAA  
lys glu ser asp gly gly lys ser lys glu lys ile glu lys leu lys leu gln ala glu  
961/321 991/331  
TCC TTC TGC CAG CGT TTG GGG AAA TAC CGG ATG CCC TTT GCC TGG GCA CCC ATA AGC TTA  
ser phe cys gln arg leu gly lys tyr arg met pro phe ala trp ala pro ile ser leu



2161/721	GTG	CTC	TTC	CTG	CAC	CTG	GTG	CTG	GAC	AAG	CTC	TTC	CAG	CTG	TCC	GTG	CAG	CCC	ATG	GTC
val leu phe leu his leu val leu leu asp lys	leu	phe	gln	thr	ala	asn	phe	ser	gln	phe	ala	phe	glu	ser	val	val	ala	ile	ala	
2221/741	ATC	GCT	GGC	CAG	ACA	GCC	AAC	TTC	TCC	CAG	TTT	GCC	TTC	GAG	TCC	GTG	GTG	GCC	ATC	GCC
ile ala gly gln thr ala asn phe ser gln	phe	ala	phe	glu	ser	val	val	ala	ile	ala										
2281/761	AAC	AGT	CTG	CAC	AAC	AGC	AAG	GAC	CTG	AGC	AAG	GAC	CAG	CAT	GGG	AGG	AAC	TGC	CTG	CTG
asn ser leu his asn ser lys asp leu ser	lys	asp	gln	his	gly	arg	asn	cys	leu	leu										
2341/781	GCT	TCC	TAC	GTG	CAC	TAC	GTC	TTC	CGC	CTG	CCA	GAG	GTG	CAA	AGG	GAT	GTG	CCC	AAG	TCA
ala ser tyr val his tyr val phe arg leu	pro	glu	val	gln	arg	asp	val	pro	lys	ser										
2401/801	GGC	GCT	CCC	ACT	GCC	CTC	CTA	GAC	CCT	CGG	AGC	TAC	CAC	ACG	TAT	GGC	CGC	ACA	TCA	GCT
gly ala pro thr ala leu leu asp pro arg	ser	tyr	his	thr	tyr	gly	arg	thr	ser	ala										
2461/821	GCT	GCT	GTG	AGT	TCA	AAG	CTG	CTG	CAG	GCC	CGG	GTG	ATG	AGC	AGC	AGT	AAC	CCA	GAC	CTC
ala ala val ser ser lys leu leu gln ala	arg	val	met	ser	ser	asn	pro	asp	leu											
2521/841	GCG	GGG	ACA	CAC	TCC	GCA	GCA	GAC	GAG	GAA	GTG	AAG	AAC	ATC	ATG	TCT	TCA	AAG	ATC	GCC
ala gly thr his ser ala ala asp glu glu	val	lys	asn	ile	met	ser	ser	lys	ile	ala										
2581/861	GAT	CGC	AAC	TGC	AGC	CGA	ATG	TCT	TAC	TAT	TGC	TCT	GGC	AGT	AGT	GAT	GCT	CCA	AGT	TCA
asp arg asn cys ser arg met ser tyr tyr	cys	ser	gly	ser	ser	asp	ala	pro	ser	ser										
2641/881	CCT	GCA	GCC	CCA	AGG	CCA	GCC	AGC	AAA	AAG	CAT	TTC	CAT	GAG	GAG	CTT	GCC	CTT	CAG	ATG
pro ala ala pro arg pro ala ser lys lys	his	phe	his	glu	glu	leu	ala	leu	gln	met										
2701/901	GTG	GTC	AGC	ACC	GGA	ATG	GTG	AAA	AGC	ATG	GCC	CAG	CAC	GTA	CAT	AAC	ATG	GAC	AAA	CGG
val val ser thr gly met val lys ser met	ala	gln	his	val	his	asn	met	asp	lys	arg										
2761/921	GAC	AGT	TTT	CGG	AGG	ACT	CGT	TTT	TCT	GAC	CGT	TTC	ATG	GAT	GAC	ATA	ACT	ACT	ATT	GTT
asp ser phe arg arg thr arg phe ser asp	arg	phe	met	asp	asp	ile	thr	thr	ile	val										
2821/941	AAT	GTG	GTC	ACC	TCG	GAA	ATT	GCA	GCC	CTT	TTA	GTA	AAA	CCA	CAG	AAG	GAA	AAT	GAA	CAG
asn val val thr ser glu ile ala ala leu	leu	val	lys	pro	gln	lys	glu	asn	glu	gln										
2881/961	GCG	GAA	AAG	ATG	AAC	ATC	AGC	CTG	GCT	TTC	TTT	TTG	TAT	GAC	CTT	CTC	TCC	CTC	ATG	GAT
ala glu lys met asn ile ser leu ala phe	phe	leu	tyr	asp	leu	leu	ser	leu	met	asp										
2941/981	CGG	GGC	TTT	GTG	TTT	AAC	CTC	ATC	AGA	CAT	TAT	TGC	AGC	CAG	CTG	TCA	GCC	AAG	CTC	AGT
arg gly phe val phe asn leu ile arg his	tyr	cys	ser	gln	leu	ser	ala	lys	leu	ser										
3001/1001	AAC	CTT	CCA	ACG	CTC	ATT	TCC	ATG	AGG	CTA	GAG	TTC	CTG	AGA	ATC	CTC	TGT	AGC	CAT	GAG
asn leu pro thr leu ile ser met arg leu	glu	phe	leu	arg	ile	leu	cys	ser	his	glu										
3061/1021	CAT	TAC	CTC	AAT	CTG	AAC	CTT	TTT	TTT	ATG	AAT	GCT	GAT	ACT	GCT	CCA	ACA	TCT	CCT	TGT
his tyr leu asn leu asn leu phe phe met	asn	ala	asp	thr	ala	pro	thr	ser	pro	cys										
3121/1041	CCT	TCC	ATA	TCT	TCC	CAG	AAC	TCA	AGC	TCC	TGC	TCC	AGC	TTC	CAG	GAC	CAG	AAG	ATC	GCC
pro ser ile ser ser gln asn ser ser ser	cys	ser	ser	phe	gln	asp	gln	lys	ile	ala										
3181/1061	AGC	ATG	TTC																	



4441/1481	TTT AAT GAA GAG CAC CTG AGA AGA TCC TTG	4471/1491	AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC
phe asn glu glu his leu arg arg ser leu	arg thr ile leu ala tyr ser glu glu asp		
4501/1501		4531/1511	
ACA GCC ATG CAG ATG ACT CCT TTT CCC ACC	CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT		
thr ala met gln met thr pro phe pro thr	gln val glu glu leu leu cys asn leu asn		
4561/1521		4591/1531	
AGC ATC TTA TAT GAC ACA GTG AAA ATG AGG	GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG		
ser ile leu tyr asp thr val lys met arg	gla phe gln glu asp pro glu met leu met		
4621/1541		4651/1551	
GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC	CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG		
asp leu met tyr arg ile ala lys ser tyr	gln ala ser pro asp leu arg leu thr trp		
4681/1561		4711/1571	
CTC CAG AAC ATG GCA GAG AAA CAC ACC AAG	AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC		
leu gln asn met ala glu lys his thr lys	lys lys cys tyr thr glu ala ala met cys		
4741/1581		4771/1591	
CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG	TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC		
leu val his ala ala ala leu val ala glu	tyr leu ser met leu glu asp his ser tyr		
4801/1601		4831/1611	
CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT	ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG		
leu pro val gly ser val ser phe gln asn	ile ser ser asn val leu glu glu ser val		
4861/1621		4891/1631	
GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG	GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC		
val ser glu asp thr leu ser pro asp glu	asp gly val cys ala gly gln tyr phe thr		
4921/1641		4951/1651	
GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG	GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA		
glu ser gly leu val gly leu leu glu gln	ala ala glu leu phe ser thr gly gly leu		
4981/1661		5011/1671	
TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG	GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA		
tyr glu thr val asn glu val tyr lys leu	val ile pro ile leu glu ala his arg glu		
5041/1681		5071/1691	
TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG	CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC		
phe arg lys leu thr leu thr his ser lys	leu gln arg ala phe asp ser ile val asn		
5101/1701		5131/1711	
AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC	TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT		
lys asp his lys arg met phe gly thr tyr	phe arg val gly phe phe gly ser lys phe		
5161/1721		5191/1731	
GGG GAT TTG GAT GAA CAG GAG TTT GTC TAC	AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG		
gly asp leu asp glu gln glu phe val tyr	lys glu pro ala ile thr lys leu pro glu		
5221/1741		5251/1751	
ATC TCA CAT AGA CTA GAG GCA TTT TAT GGT	CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG		
ile ser his arg leu glu ala phe tyr gly	gln cys phe gly ala glu phe val glu val		
5281/1761		5311/1771	
ATT AAA GAC TCC ACT CCT GTG GAC AAA ACC	AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG		
ile lys asp ser thr pro val asp lys thr	lys leu asp pro asn lys ala tyr ile gln		
5341/1781		5371/1791	
ATC ACT TTT GTG GAG CCC TAC TTT GAT GAG	TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT		
ile thr phe val glu pro tyr phe asp glu	tyr glu met lys asp arg val thr tyr phe		
5401/1801		5431/1811	
GAG AAG AAT TTC AAC CTC CGG AGG TTC ATG	TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG		
glu lys asn phe asn leu arg arg phe met	tyr thr thr pro phe thr leu glu gly arg		
5461/1821		5491/1831	
CCT CGG GGA GAG CTG CAT GAG CAG TAC AGA	AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC		
pro arg gly glu leu his glu gln tyr arg	arg asn thr val leu thr thr met his ala		
5521/1841		5551/1851	
TTC CCC TAC ATC AAG ACC AGG ATC AGC GTC	ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG		
phe pro tyr ile lys thr arg ile ser val	ile gln lys glu glu phe val leu thr pro		





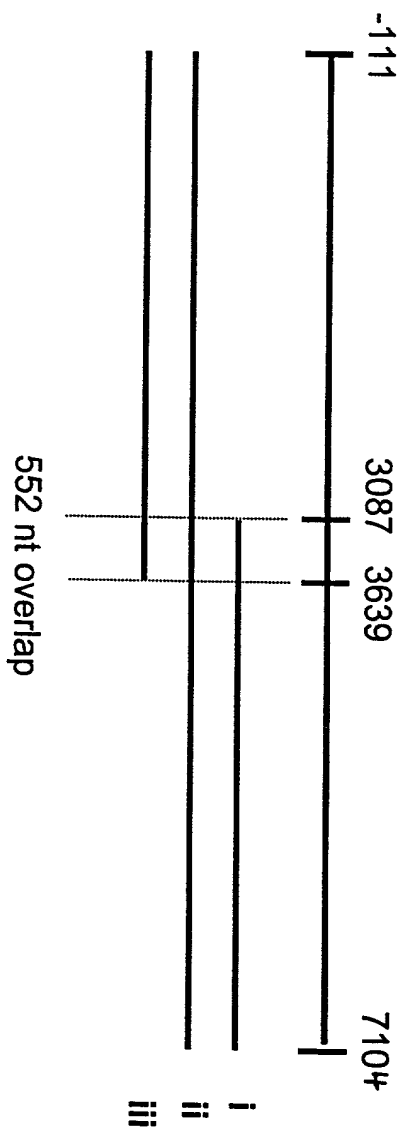
[illegible]

### B. Alternative splices

These differences may be found separately or together in various combinations in the different human CLASP-5 isoforms

FIG. 6

nucleotide numbering  
as in Figure 6A



C

[illegible]

002427 09636260

1<sup>st</sup> partial exon (nucleotides 3793 to 3952)

CCAGCTGTCAGCCAAGCTCAGTAACCTTCCAACGCTCATTTCATGAGGCTAG  
AGTTCCTGAGAATCCTCTGTAGCCATGAGCATTACCTCAATCTGAACCTTTTT  
TTTATGAATGCTGATACTGCTCCAACATCTCCTTGTCCTTCCATATCTTCCCAG  
GTAATAAAAGAATTATTTAACTAAAAGAATTATTCAAGCTAT

2<sup>nd</sup> exon (nucleotides 5809 to 5948)

GCTCATAAAATGGCTCCTTACGTTTCTGTAGAACTCAAGCTCCTGCTCCAGCT  
TCCAGGACCAGAAGATCGCCAGCATGTTTCGATCTGACTTCCGAGTACCGCCA  
GCAGCACTTCCTCACCGGGCTCCTCTTCACAGAACTGGCTGCTGCCCTGGATG  
CCGAAGGGGAAGGGTATGTTTCTGGCATTAAAATGGAAGATGAAGC

3<sup>rd</sup> exon (nucleotides 13662 to 13831)

CATAACCTCTTGATTCTGTGTTGTGCCAACAGAAATCAGCAAAGTACAAAGG  
AAAGCTGTCAGTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCAC  
GCTGTGTCAAACCAGAGGTGAAGGTCAAAATCGCCGCCCTTTACCTACCTTTA  
GTTGGCATCATTTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGGTAATGG  
CCCTTCTGTTTTCTTTCTTGGATTG

4<sup>th</sup> exon (nucleotides 16948 to 17087)

TGTTTGACTTGACATCACAAACGATGTTTTATTGCAGTTGCAGATACTCGCA  
GATACCGCACCAGTGGCTCGGATGAAGAACAAGAAGGAGCCGGTGCCATTA  
ACCAGAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAG  
TGGAATAGTGCTGTCTTCCTTGGTATGTTGGTGCACATGTGTCTGGTTGATTTT  
TCAT

5<sup>th</sup> exon (nucleotides 19281 to 19463)

TGGCCTCCATCCCCCAATCTGCCTCCCTTCAGCCCTATAAGCAGTACAACATG  
CTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCCTCTGGATCATGAA  
AAATGCTGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACG  
CAGCTCAACAGGATTTTAGATCTACTTTTCATCTGTGTGTTATGTTTTGAGTAT  
AAGGTAAGTCTGGAGTGGCACAACCTTTATACCAGC

6<sup>th</sup> exon (nucleotides 19829 to 19958)

CACCAAAGGACATGTCCTCCTACCTCTGTCTTGTCAGGGGAAAACAGAGTTCT  
GACAAAGTCAGTACCCAAGTCCTGCAGAAAGTCAAGGGATGTCAAGGCCCGG  
CTGGAAGAGGCTTTGCTGCGTGGGGAAAGGGGCCAGAGGGGAGATGATGCGC  
CGCCGGGCTCCAGGTGTGTTGGACTGGCCCTTCCCTGCTCTCTGTCAAGC

7<sup>th</sup> exon (nucleotides 20928 to 21015)

TCAAATTCCTATCATGCATTTCTTAACTCCTAGGGAACGACCGATTTCAGGC  
CTAAATGAAAATTTGAGATGGAAGAAAGAGCAGACACATTGGCGGCAAGCT  
AATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTTCTGCTACTTTTACCT

8<sup>th</sup> exon (nucleotides 25765 to 25861)

GCTTTAATTTGACCTCTTGTTGTTTCCTAGAACAAAGGCCGAGTTAGATCAAG  
AAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCCTGGA  
TATGCAGGAAAACATTATCCAGGTGAGGAAAACAAACACCCAATCTGATTG

9<sup>th</sup> exon (nucleotides 27242 to 27376)

GGATTCAATGATGCTGTTCTTCCATTCCCCCAGGCGAGCTCGGCTCTGGACTG  
TAAAGACAGCCTGCTGGGAGGTGTTCTGAGGGTGCTGGTGAATTCTCTGAAC  
TGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCGTGCTCT  
CATCGCCAAGGTAAACTTGGGATGCTTGTTTTCTTCCTCTTAATT

10<sup>th</sup> exon (nucleotides 28582 to 28734)

AGTGATGCCTAATGGCCCTTTATGTCTCTCCTAGTTTGGGAGACTTACTCTTCG  
AAGAGGAGGTGGAACAGTGTTCGACCTATGTCACCAAGTCCTGCACCACTG  
CAGCAGCAGCATGGATGTCACCCGGAGCCAAGCCTGTGCCACCCTTTACCTC  
CTCATGAGGTTCAGTTTTGGAGCCACCAGTGTAAGAGTTCAAACCAGCTGAG  
TGACCTGGAATCAG

11<sup>th</sup> exon (nucleotides 31046 to 31204)

TTACTTCATCTTTTTTTTTTTTTTCACTGATGCAGAAATTTGCAAGAGTAAAGA  
TGCAAGTAACCATGTCCCTGGCATCTTTGGTGGAAGAGCACCAGACTTTAA  
TGAAGAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTCAGAAGAG  
GACACAGCCATGCAGATGACTCCTTTTCCCACCCAGGTACACCGAAGCACAT  
ACCTTGTCTCATGCATGAGT

12<sup>th</sup> exon (nucleotides 32755 to 32855)

AGCTAAGATTATTTTGAGGCTTACACTTTTTGCAGGTGGAGGAACTTCTCTGT  
AATCTGAATAGCATCTTATATGACACAGTGAAAATGAGGGAATTCAGGAAG  
ATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCCTGACACACTCA  
AGGGACACCATTT

13<sup>th</sup> exon (nucleotides 33663 to 33855)

TCCTCAAACTACTTCTCACTCAATCTGTCTTCAGAAATTGCCAAGAGTTACCA  
GGCATCTCCTGATCTGCGGCTGACCTGGCTCCAGAACATGGCAGAGAAACAC  
ACCAAGAAGAAGTGCTACACGGAGGCTGCCATGTGCCTGGTGCACGCCGCTG  
CGTTAGTGGCTGAGTATCTGAGCATGCTGGAGGACCACAGCTACCTGCCCCTG  
GGGCAGTGTGAGCTTCCAGGTAGGGTGTGTGCAGCTTTTCCCTTAGAGCAGTG  
GTTC

14<sup>th</sup> exon (nucleotides 38125 to 38268)

CTGTTCTCCAGGCTTATACTGTGGTCTCTTTCAGAATATTTCTTCCAATGTGCT  
GGAGGAGTCTGTGGTCTCTGAGGACACCCTGTCACCTGACGAGGATGGGGTG  
TGCGCAGGCCAGTACTTCACCGAGAGTGGCCTGGTAGGCCTCCTGGAGCAGG  
CCGCGGAGCTCTTCAGCACGGTCAGTGCCAGAGGGCATCCCGGGGCCTGGC  
C

15<sup>th</sup> exon (nucleotides 40166 to 40297)

AATTCTCTCTGATGCTCTTCTCCTCTTTCCAAGGGAGGCTTATATGAGACAGT  
TAATGAGGTCTACAAGCTGGTCATCCCCATCCTAGAAGCGCATCGAGAATTC  
CGGAAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCG  
TTAACAAGGTAGCCGGGGAGCCTGGCTGGCAGGTCTTGTTAC

16<sup>th</sup> exon (nucleotides 40755 to 40889)

TAAGGAGAGCTTTTTATATTTTGTTCCTCAGGATCATAAGAGAATGTTTGGAA  
CCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTGATGAACAG  
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG  
ACTAGAGGTAAGAAAAGTGATTCTGTGCGCCTGACCTGGTACACTTTAC

17<sup>th</sup> exon (nucleotides 42307 to 42396)

AACCTTTATAAACTGTTGGTTCTTCTTACCTAGGCATTTTATGGTCAATGTTTT  
GGTGCAGAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA  
AGTTGGATCCTAACAAGGTATACAAAAATTTACAAAACTAACCATCAAGC

18<sup>th</sup> exon (nucleotides 45250 to 45486)

TCTTCTCCCTCCGTGCCTTTTCCCCCTTAGGCCTACATACAGATCACTTTTGTG  
GAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGA  
AGAATTTCAACCTCCGGAGGTTTCATGTACACCACCCCGTTCACCCTGGAGGG  
GCGGCCTCGGGGAGAGCTGCATGAGCAGTACAGAAGGAACACAGTCCTGAC  
CACTATGCACGCCTTCCCCTACATCAAGACCAGGATCAGCGTCATCCAGAAG  
GAGGAGGTAATGCACCCAAGGGATTGGCCACCACTGGATGAGT

19<sup>th</sup> exon (nucleotides 48664 to 48807)

ACAGTGA CTTCCTATGTTTACGTCTCATGTTTCAGTTTGTGTTTGACACCGATTG  
AAGTTGCCATTGAAGACATGAAGAAGAAGACCCTGCAGTTAGCAGTTGCCAT  
TAACCAGGAGCCGCCTGATGCAAAGATGCTTCAGATGGTGCTGCAAGGCTCT  
GTGGGAGCTACTGTAAATCAGGTAAGCAAAACCAGAGGTGGCAGCTCCT

20<sup>th</sup> exon (nucleotides 50892 to 50998)

TATATTCTTTTTTTTTTTTTTTTTTTTTTCCCAACAGGGACCACTGGAAGTAGC  
CCAAGTGTTTTTGGCTGAAATTCCTGCTGATCCAAAACCTCTATCGACATCACA  
ACAAGTTGAGGTTATGCTTTAAGGAATTCATCATGAGGTAAGAAGGAAAATG  
GCTGGGAATTCAGTAGAG

21<sup>st</sup> exon (nucleotides 62398 to 62568)

TCATTTATTTCTCCCACTGATATTTTCATCTCAGATGTGGTGAAGCTGTAG  
AGAAAAACAAGCGTCTCATCACGGCAGACCAGAGGGAATATCAGCAGGAAC

TCAAAAAGAACTATAACAAGCTAAAAGAGAACCTCAGGCCAATGATCGAGC  
GGAAAATTCCAGAACTGTACAAGCCAATATTCAGAGTTGAGAGTCAAAGAG  
GTAAGAACAGGGCAGAGGAGGCCTCTTCCTGTGGGAT

22nd exon (nucleotides 63040 to 63294)

CCTCCCTCTCTTTTCTTAATTTTCAGGGACTCCTTCCACAGATCTAGTTTCAGGA  
AATGTGAAACCCAGTTGTACAGGGCAGCTAAGAAAAGCCATCTTCATTCGT  
GGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAAT  
GGGACATTTGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTC  
TGGAAGCTTTGGGATCCCAGGAACCATGGAATTATCCCAAATGGACTCTGA  
CCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGC  
ATGACTGCGTATTTATTAAAGTGTGTTTTTCCACAATGTACCAAACAAGGCAT  
AAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATCTGAGAGATGATTTC  
CTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTGCCTGAGGAAAAAT  
GGAAAAATTATCCACCAGTCGATTCAAACCTGAATTTCACTCTTTATAGGAAG  
GCAGGGCAAACCTGTAGGAGTACGAAACATTTTCAATAAATCTACAAAGGGA  
AGCCTTACTACAATTCAAAAAATCATCATGGTTGGAAATTTGGGAGGAGATT  
ATTTGTGAACCTTGTTACCCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTAT  
TTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTATAGAAGAATAC  
ATCAAAGCACTGATGTAGGAGATACACGGTACTTGGAGCAGTCAGCCAAAA  
ATCACAGATACTGCTTTCACTTAAATGGAAACAATTCTCCGATAATGCTTTGC  
TTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTTTCTCCTCTCTGGGACCAA  
GTTTCTTTTTTATAAAGCAATAATATCTCTGTTTTTCATTTCAGAACATTGTGCTG  
TCTGTCAGCATATGTATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTG  
ACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTGAGAATTAAATT  
ATATATTTTTAATATGACTGTGACCTTGACTGATAATAAAGATGTAATAAGAA  
TTGCAAGCTAAAAAAAAAAAAAAAAAAAAA





4551 TCAGTAGCTCAGAGCATCAGGCAAAATTTCTCATTATTAGGTTATATTTCTGTTGCATATTCTTGATACTAGTACAAAAGTGAAGGCTTG  
 4642 TCTTACTAATTGAAAAAAATCTTAGCCATATATGCCATATGGCATGATCCAGATATTAGCTACATGACCATCTTACTGTGAACAGGGAA  
 4733 AGATCTGACTCACAAAGCAGCAATTCAAAATGTATAAACTTTTTTGCTCCATCCTGCCAGCAGCTTAAGTCCATAAACTTCCCTGGACTAAG  
 4824 CTTACCCCTAGGTTCTTTCCACCTTCCCCTTCTGACTGCCCCAGGGAGTGGCCAAACCCAGGGGCCAGGCTCACAAAACCATGAAGGATTT  
 4915 CTAAAGACACTTTAGATGCTCTTAATGAAATATAAAGTGTGCTCCAGGATACAAATACAGGACAGGAATTACTGAGGACCGGTAAATCTA  
 5006 ATACTTCCCCTCCCTGACATCACTTGTAGTTCAGGCCAGCAAAAGTCTGACAAATGTGCTTAAGCCAAATTGAGAAGTGTAGCTGAGGCCG  
 5097 GCACGGTGGCTCACATTTGTAATCCAGCATCTTCGGAGGCCAAAGGGAGTGGAAATCTTGAGGCAGGAGTTACCAGCCTGACCAACATGA  
 5188 TGAAACTCATATCTACTAAAAATACAAAAATGCATCAGGTGTGGTAGTGTGACTGTAATCCAGCTACTTGGGACGCTGAGGCATGAGAA  
 5279 TTGCTTGAAACCCGGGAGAGGGAGGTTGCAGTGAGCTGAGACCATGCCACTGCAATCCAGCCTGGGTAAACAGAGTGACACTCTGTCTTTCAA  
 5370 AAAAAAAAAAAAAAAAAAAGAAGGTACCTGAGTAAGCAGGGCCTTAAACAAGGGGGCATTTGGTTACAGAGGAATTGCCTGTTCCCAGC  
 5461 CCCAGGACTGGGTGAGGTTCTTATTTCTCTGTCCAACCTTTTATGCTAGGATTTTATCTTCAGCTTTTGATTTACAGTGAGGAAAGGAGCG  
 5552 TCATTCAATTTTTCAACAGACCCGGGTGCTTTATTTTCATCTTTCCCGCTGGGCAGTCTTCTCTCTGTGGGTATGGGAAAGTGCAGTAACC  
 5643 ACTCTGTGCCTCAGTTTCTTGTCCGCTTATCTGGCACCAGAGTACCTACCTCACTGGGGAGGGCTCACGAAGCCTGGCTGGGGCAGGA  
 5734 CTCAGTAAACACTGGCCATCGCTATTTTCATTCCAGTCTTGTGGCTCATAAATGGCTCCTTACGTTTCTGTAGAACTCAAGCTCTGCT  
 5825 CCAGCTTCCAGGACCAGAAGATGCCAGCATGTTGATCTGACTTCCGAGTACCGCCAGCAGCACTTCTCTCACCAGGGCTCCTTTCACAGA  
 5916 ACTGGCTGCTGCCCTGGATGCCGAAGGGGAAGGGTATGTTTCTGGCATTTAAATGGAAGATGAAGCCAAAAAACAGATGTTCTTTAATA  
 6007 AAATTTGCAGTCTAGCTTCTCACACTTGGTAAAAACTCTACTGTAGTTGACCAGTCTGAGGAGTAGAAACATCTGTCTTGAGAAATATGG  
 6098 TACCCATAAGCACAAAGGCACAAGAAAGCCCTTCTTGTGTAGAAAGGCACAGGGATGGGTAAAGAACTACAAATGACTTTTCTTGGTCAA  
 6189 CTATTTCACTGGAATTTACCAAGTCTGCTATAGCAGGTTTCCCAAGGATGCTTTGATTAGTGAATCCCTAGGAGCAAGCCATTTTAAAC  
 6280 AAAGGGATAGCATGCAGAGGCAACCACAAGATGTCACTTGGTTCAAAGCTGATGAAGGAAATATGGCTGCTGAGAAGGCAGCTGTCCCA  
 6371 TGCCAGATTAGGTTTCTTGCAGACAGTGCTTCTCAGGCCAAGAGACACCACATCCAGGGCTTCTGAATCCTTTTACCTCTTATCTATC  
 6462 TGATTACTCAGGGACATGTGGCAGTATCTAGCCTAGAAGTCAACAGACAGAGAGGTAGACCACCCCTTCTTCCCTCTCTCCCTATGCTC  
 6553 CGTGAGCTCATGGAGTCAGAAACCCACAGCCTATCTGATTGGACTGAAAAAGATAATGCCTTCTAAAATATTATTCAATCCGTTCAACAAT  
 6644 TATTGAATGCCTTCCATGGGACAGACAGTGTAGGTGTTAGAGTACATCAGAGATATATCAGTGCACAAAACAGACAAAATTCGCTGCCCC  
 6735 TCAAGAGCTCACCATCCAGGGACTCAGATTCAAAGATGATTAGGATTGCAAAGTAGTTGAGATTCAACACTTCTGGTGTGTTAGATTAGCA  
 6826 TACAGAATTGCAGGAACCTGCCCACTATTCCATAACAGAGAACGAAATCTAAAGCCATGGTCTTCCCAGTCCCTTCCCAGGACCCACTCTC  
 6917 CTATACCAAAACCATCTCCCTGCACAGGGAACCTGTTCCCATGACTCCTATGCTAAAGAGGTTTCCAGAATAATGTTTGCTAATTAATGGTA  
 7008 GCATTGCTGTATGTTATGGATGGATTTTTATCTAAATGGAATTTCTCAAGTCTCTCAAAGTGTCTTACAATTTAGTGAAGGAAACAGGAGG  
 7099 TTCCTGCATGAAACAAATACAGGAGCACATCGAGTTCGTGCAACTGCAACAGTCACATGTGTCCCAAGCTATGTACCCAGGCTGACACCGC  
 7190 TGAAGTGAATCTATGTCTGCGTCTCCTGGCAGGATAGTGTGGGGAATCTCATGCTTTTAGCTCTCAATTCGCTCCTTCCAGATAAACTG  
 7281 GCCTGAGTATATCCTTTGAGAATTCACCTTCCATGGCTTCAATTCATCTCTCTTCACTCTAACTAAATTTCTCCCAATTATCTCA  
 7372 GTAGAATGTTCTACCCTACAACPAACATAAATTTCCACAGCAACAAAAGTGACCCGAACACTTATGCTAATAAGTAAGTACTGAGAAGA  
 7463 AAGTTTGAACACAAAGAAAATTGCCCTTATGCAACAAACATGTACATACATTTTCTTAGTTGTCTTTAATAGCAGTACTTTAAGTGATTTT  
 7554 TAGAAACATCTTTAGTATTTACAATAGCGTAGTTCTATTTTCTATTTTCATCTAGCTGGAACAGCCATGACATTCTGTTCTGGATTCC  
 7645 TTGTAATAATTGTTGCTGTTATATTACTAGCAACAAGGTAGAGTATATTAGAGATAATCATGTAATTATGTTAATCAGGTAGATACATTC  
 7736 TTCAAACACACACACACACACACACACACACGCGCAGTGCATGCACACACAGTACCTTTCTCCCCAAAGAGTAATTA  
 7827 ACAGTGAATCCTTTGGCAACACAGTAATCCCTGATTGCTGGGTGTGAGTACTCTCTGGAAAGTCATTAGATACACTGTACAACTT  
 7918 CATCATGTAAGCTAAAACCTCAGAAAAATGTATGCTTCAACAATACTTCTTATTGATCAGCACTTCCCTTTTTTTTTTTCTTTGCTTCCA  
 8009 AGACAGTTGGTAGACTTGCCAAACCTGTACATCCATGGGGCAAGGGCCAGAAGGACGCATCTCAGTACCTGAACCCCTAGGGAGCTACAG  
 8100 CTCAGTTTCCACTGGGTTTCCCTTGGATCTCTGACACCTGGGTATATCCACAAGTGTCTATGCATCGTTAAATCCACAGTGTTTTCAAG  
 8191 CATTTAGAAATTGCTATCATCTTTGTGTTAAGCCAGCAAAATGCAATGCCAATTCAAACACAACCCATTGCCGGGACCACAGACTAAG  
 8282 AACAGAAAAACTTTTGAAATGCAATTTACAATTATCTTACTTTAGCCACAGTGCAAGAGTCTGAGTCAATTTAAATTTTGGTTAATATTT  
 8373 TCTATATAACGTTGAATCTGATGTAGCCTATTTTGTGTTGAAAGAAAAAATGTATATATATGTATATATTTTTTAAATCTGGATTCTTT  
 8464 TTTTATATTATCACTTTAAGTCTAGGGTACATGTATACAACATGCAGGTTTGTACATATGTATATATGCGCCATGTTGGTGTGCTG  
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 8737 CTACAAAGGACATGAACCTATCCTTTTTATGGCTGCATAGTATCCATGTTGTATATGTGCCACATTTCTTAATCCAGTCTACCAATTGA  
 8828 TGGACATTTGGGTGGTTCCAAGTCTTTGCTATGTGTAATAGTGCCGAATAAAAGGATTATAAATCATGCTGTATAAAGACATATGCAC  
 8919 ACATATGTTTATGCGGCAAGATGTATATTTTTAAATTTGAACATCTATGACTAGGTTCCAGATACTCCACTATATATTTTATTACTTTT  
 9010 TATTATAGTATAATTTATATAAAGAACCTGAATCCTAAGTGTAAGAGTGCAGTAAATTTCTGTGAATATATTTGAGTAACCACCACTC

9101 AGATAAAAAATATAATATTCCATTATCCTCTCTCAGTTACAGGCCCCCTCAAGTAACCACTATTCTGACTCTTATTATTAGAAATTAATA  
 9192 CTGCGCTGTTGTTGAATTTTCATAGTCTTTTGCTGAATGTTGTGACTGTGACATCCTTTAGTGTGGTTCGCATGTGTCACTATTATTTTTTTT  
 9283 CAACTGTATGTCATAATTCCTTTGTCTACTATAATTTCTCTTCTGTAATTTGACATTTGGGCTGCTTTTCTATTTGTGGGTATTGGGTATTAT  
 9374 GAAACAGCTGCCGTGAACATGCCTGTGCATGGTTTTGGGTGGACGTTAGAACTCATTTCTTTGGGGCTATAAATACAGCCTATTTTTTAT  
 9465 TTTAATATACTGCTCTTGAATAGTTTAAATAAATATGTGTACATGGTCTTAACAAAATGTCAAAGAATATACTCTGAGCTAGGAAAAGAAG  
 9556 AGCAAACAAGTCAAAGCAGGAAGATGGCAGGGAATAACAAAGGTGATAGCCAAAATAAATGAAATAAAGAATAGAAAAACAATCACGGAAA  
 9647 TCCGCAAGATGAAAAGCTTGTATTGTAAGAGCAACAAAATTCACCAATCTTTAGCTGAGCTGACCAAGAAAAAGGAAGAAGACTCAA  
 9738 TTACTAAAATCATAATTGAAAGATTCAACACAATCATATACAAGAGACCTTACAGAAATAAAAAGGATTATAAAGAATACGATGAACAA  
 9829 TTGAAAGCCATCAAATTGATAACCTAGATTAAATGGATAAATTCCTTAAAGGTACAAAGTACTAAAATTGACTCCAAGAAGATATAGAAA  
 9920 ATCCAAATAGACCTACAGAAGTAAAAGATTGAGTTAGTAATCAAACCTCCACATACACCTACTATGTACCCACACAAATTAATAATTTA  
 10011 GGCTGGGCGCAGTGGCTCATACCTGTAATCCAGCACCTTTGGGTGGCCAAGGCGAGTGGATCACCTGAGGTCAAGAGTTCAAGACCAGCCT  
 10102 GGCCAAGGTGATGAACCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGTGGCGGGAACCTGTAATCCCATCTACTCGGGAGGC  
 10193 TGAGGCAGAGAATCATTTGAGACTGGAAGGCAGAGGTTGCAGTGAGCCAAGATCATGCCAATGCCTCCAGCCTGGGCAACAAGAGCAAA  
 10284 ACTCCATCACAAATAATAATAATAATAATATATTTTTAAATTTAAACTTCCTACAATAAAAGCTCAAACCTGGGGGGCTTTACTGAT  
 10375 GAATTCTACCAATAATTTTTAAAGAATTAATTTCTAATTTTTTACCAACTTCCAGTCTTCTCTTCCAACGAATGGAAGAGGTGGAATACTT  
 10466 CCCCCTTGTCTATGAAGCTAGCATTACCCCTATACTAAACCAGACAAAGACATCATGAGAAAACCTACAGGCCAGTATCTGATGAATATAG  
 10557 ATGTAAGACCTCAACAAACACTAGCAAACTGAATCCAACAGCATATAAAAGGATTATACACCATGGCTAAGTAGGATTATCTCAGGAA  
 10648 TGCAAGATAGGCTGCATACCTGAAATCAATTGTTGTACCATATTAATAAAATAAAGGACAAAACCCATACAATCATCTTAGTAGATGCAA  
 10739 AGAAAAGCATTTAATAAAATCTAATAACGCTTCTGTATAAAACACTCAACAAACCTTTTAGGAAATAAGAGAATTCCTCAACTTGACTT  
 10830 AAGGGCCTCTATGAAAATCCACAGCTAATGTGACACTTATTAGTGAAAACAGTGTCTTATCCCTAAGATTAGGAACAAGACAAAATGT  
 10921 CTACCCCTTGGCACTTCTATTCAACATAATTAGGAGTTCTATCTAGGGCAATTAGGCCAAAAAATAAACAAGACATCTAGGCCAGGCGTG  
 11012 GTGGCTCACGCTGTAAATCCAGCACCTTTGGGAGGCCAAAGTGACAGATCGCTTTGAGCCAGGAGACTGAGAACACCTGAGCAACATG  
 11103 GCAAAACGCCATCTCTACAAGAAATACAAAAATTAGCTGGGCATTGGTGGCTTGTGTTGTAGTCCCAGCTACTTGGGAGTTGAGGCTGG  
 11194 AGAATTGCTTGATCCAGAAAGCGGAGTTGTAGTGAGCTGAGATCACGCTACTGCCTCCAGCCTGGGCCACAGAGTAAGACCTGTCTC  
 11285 AAAAAAAAAAAAAAAAAAGAAAAGAAAAGAAAAGAAAGCATTAAATTGGAAGAAGTAAACTATCTCTATTCATAGGTGGCATAA  
 11376 TCTTGTATTATAGAAAACCATAAGGAATCCACAAAAACTCCATTACAATAATAAATGAATTCAGCAGTGTTCATGGTATAAGATCAACA  
 11467 TACAAGAAATCAATTGTGTTTCTATACACTTACGATGAGCAATCTGAAAATGAAATTAAGAAAACAATTCATATAAAATAGCATCACAAAG  
 11558 AAAAAATATTTAGGAATAAATGTAACAAAAGAACACAGAGTTATACACTAAAAATGACAAAACACTGTTGAAAGAAAGATATAAATAAA  
 11649 TGGAGGATATCATATGTTTCATGAATCAGAAGACTTATTATTAATAATAGCAATCTCCCAAAATGATCCATAGATTAAATGCAGTTCTTCT  
 11740 CAGAATCTAGCTTGCTTTTTTTTTTTTTTGGCAGAAATTAGCAAACTGATCCTAAAAATTCGTGTGGAATTCAGGGACCCAGTATAGCC  
 11831 AAAACAACCTTGAAAAACAAGAACAAATTTGGAGGACTCACACTTCCCAATTTCAAACTTACTACAAAGCAAAAGTAGTCAAGACTATGG  
 11922 GGTCTGACATATGATAGACATATAGATCAATGAATTTGGGTAAAGAGTCCAAAAATAAATCTTCATATTATAGTCAATTGATTTTTGAC  
 12013 AAGAGTGCCAAAACAATTCAATGGGGGAAAATAGAAATTTCAATAAATGGTGTGGGACAACCTGGGTATCCACACTCAAAAGAAATGAAGTT  
 12104 GGACCTATATTACACTGTATACAAAACTAACTCAAATAGATCAAAGACCTAAATGTAAGAGCTAAACTATAAAATTTGTACATAAAAT  
 12195 TATAGAGGTAATCATATAGACTTAGAAAAGGCAGTGGTTTCTTAGATATGACACACTCGAAAGTATGAGTAACAAGAAAAAATAGATAA  
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 12377 AAATCAAAACCTAATAGGGGACTTGTATCTGGAATATATATTTTAAATCTTACAACCTCAGTAATAAAAGACAAATAACTCAGTTTTTT  
 12468 AAAAGGCAAAAGATCAGAAATAGACATTTCTCAAAGAAGATACAGCCATAAGACCATGAAGATGTTTCAGCATCATTAGCCGTCAGGGAGAT  
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 12650 TGGAGTCTTCAGACACTGCTGGTGGGAATGTAAATTTGTGCAGCCACCGTTGAAAACAACCTTGCTGATTCTCTAAAGTTAAACAGAGGC  
 12741 TGGGCGCTCGGGCGGCTCACGCCCTATAATCTCAGCACTTTGGGAGGCTGAGGTGGGCAGATCATTTGAGGCCAGGAGTTTCAGACCAGCCTG  
 12832 GCCAAGATGGTGAACCCCTGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCAGGTGCCTGTAGTCCCCGCTACTTGGGAGGCT  
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 13014 AAAAAAAAAAAGTTAAACAGACAGTTACCATACAAGCCAGCAAAATGACTCTGAGGTATGTACCAAGAAAAGTAAACTTAAACTTGT  
 13105 ATACACATACTCATAGCAGCGTTGGTAAGTCACAATAGCTCAAAGCAGAAACAATCCAAATGTTTATCAGTTGATGAATGGATAAAATTC  
 13196 ACCAATGGAATATTATTAGCAATAAAAAGGAATGAAGTACTGATGCTACAATATGATAAACTTAAAAACATCATGCTAAACAGCAGACCC  
 13287 AGGGTTAGAACACAGGCAGTCTGTTTCTGGATTCTATGTAGTTCTATCCTATATTGCTTGGTTTTCCAGGGTTAGAACACAGGCAGTCTGT  
 13378 TTCTGGATTCTATATAGTTCTATCCTGTATTGCTTGGTTTTCCAGGGTTAGAACACAGGCAGTCTGTTTCTGGATTCTATGTAGTTCTATC  
 13469 CTGTATTGCTTGGTTTTCCAGGGTTAGAACACAGGCAGTCTGTTTCTGGATTCTATGTAGTTCTATCCTATATTGCTTGGTTTTCCAGGTC  
 13560 ACCTCATTGCTTAGGAGCGTTTTTCATCACTCTTGACTGTTTAAAGAGCTCTTTAGTCAATTTCTTTACCATAACCTCTTGATTCTGTGT

13651 TGTGCCAACAGAATCAGCAAAGTACAAAGGAAAGCTGTCACTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCACGCTGTGTCA  
13742 AACCCAGAGGTGAAGGTCAAAATCGCCGCCCTTTACCTACCTTTAGTTGGCATCATTGTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGG  
13833 TAATGGCCCTTCTGTTTTCTTTCTTGGATTGTTGGGGGCCCTGCCAAATGCCCCATCCGAATGAGATCTCTGTCAATTCGTTCCAGTGCTG  
13924 ATATGTTTCATATGAGCAATTCITTCACAAAATGGTCTCCAAACCTCTTTAACACTGGCCCCAATCAGTTAAAAAACAACAAAAGTCACAT  
14015 AGCCCCATATGTGTTTTTTGTTTGAAGAAATATTTACTTGTTCCTTCATTCAATTCATTATTTCATTGATCTGCTAGTATGGAATGAAC  
14106 TTTATAAACCATACACCACAAAGGATGAAATAATAACAAGATTACTGCCTTTGGAGATCGTGCTCTAACACCTTGAAATAAAGGTGTCTCT  
14197 TCCCTTTTCTTTTATGAATATGTAAGCAAAAAGCGGTCTCAAATGAACCCAACTAATTTGCTCCATGCAAAAAAATCATGGCATATGT  
14288 CAATATTAGAAAATTCATCATAGCAGAGAAATATTGCCCTTGGCACTAAGTACTAATTTTGAGGTTAATATGTCTAGATTAGCAACAAG  
14379 ATGAAAGGATAAGTTGTCTTAAAGGGGTTTTGTGAAACCCAGAACTATTTTACAAATTACATTGTGGATTAAAGGAATGTAGAGGGAAAAA  
14470 AATCCTCCCAATAGAGAAGCTTCTTATGTTGACCTGAGAAAGGCAGTCCATTGGCCTACCCTCTCCACAGCGTACGTGTGTGTGCACGTG  
14561 TGTGCGCGCGTGCACACACACACACAAATTCCTATCCCATCAGAGTAGTTCTTGCTTTTCTCCAGCTCAAGGGAAGTTTGGAAATG  
14652 TCCATGCTGCTCTCTTGGCAGCTGAAGGGTGTGGGATCTGGGCAATGCTTCCCTGAGCCAGCCTCTTTATAGTCAGTCATCCTTGAATC  
14743 TTGGAACCATCCAGGTTTTCCACCTCTCCAAATGGAAAGTGTCTATGTGTGACTAATTTGTTTATAATACTATTACGGTGACAAGTATTT  
14834 AGTTTCATGAAATGGGACCAACGCCCTATAGTCTTTAATTCATACAAATCATAAAATGAAAAGCAAGTATTCCTGTGGAAGTAATCTCTC  
14925 CTTTCTTGAAAAAATCCTCTAGCAAACTGCTAATGGAGTAACTCAGAAAGAGAAAGGTTGAGACAGGGGTTAGGGTTTGTAGAGTTCTGTT  
15016 GGGGCCAGAGTGCAAGGAAATGATAGAAACAAGCTCAGCACACAGGGCTGAGCAAGCTGCACCATGAGGTCAGCAGCTTCTCTAGCAGCG  
15107 CCTGATTGCGCGGAATTGAAAATGGAGTTGTTTTTAAACATTACAGACATAATGCAGAGCATGGCATGTGACTTTGTAGCCATTTTGTAGAA  
15198 TCCTTGATGGCAAGTTTTCTAAAAAGTTCCATTTCAAGAGCTTGCTTGTTCCTTCCAAAGCCAGGAACCACTTTAGCACACATTATCCGAAGTTT  
15289 TCTTGTCATTAGAAATATTCGATCAGTGACTCGGAATCAGAATTTTCAACATTTGGTCTCCAAGCCTTTTAAACCTCAAAGACTTCTT  
15380 TGTATATGCGTTGAACCTTTATGATCATGATGTAGCTGATGAGAGAAAAAACAGTGAAAGTATTTTATTGTTATAGGTTACACAGTACAT  
15471 CTATTAAATATGGAATCTTTAGGTTGATAAACTCATAAGAATACAGTCTTTCAAAGATGCATCTGAATTCAGATTCCAGCCCCATTTAT  
15562 TAATATAAGTGACCTTTTGAAGGCTCAACCTTTCCGTGCTTCCCTTTCCCTCTGTAACATATAAAATGTGATAACGATGTCTACCTTTTAG  
15653 GTTTACGATAAAGGTGAACTAGAGAATCTCTATAAAGCATTTTGCACAGCAGATGTTGTATCTTTCCGATTTTCTGTAACTATAA  
15744 CCCTATGGCAATTAAGGGGAAATAAGAATGTGCTCTATGTTAGTTGTGATAATGTTATCAGGTCTTGCAATAATTTCCATGTGCTGTTTAT  
15835 TTAACCATTTGTTTAAATCCCAATGGCCTTAATAAGTATTTCTAAAAATGGGTTTTGGCTCGGTGTGGTGGCTCACCCCTGTAATCCCA  
15926 GCACCTTTGGGAGGCCAAGGTGGACAGATCACTTGAGGCCAGGGGTTCAAGACCAGCCTGGCCAAACATGGCGAAACCTGTCTCCACTAAAA  
16017 ATACAAAAGTTAGCCAGCGTGGTGGCGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGTAGGAGGATGGAGGGGAGAGATTGCAGTG  
16108 AGCGGAGATGGCGCCACTGCACCTCCAGCTGGATGATAGTGTGAGACTTTGTCTAAAAATAAATAAATAAATAAATAAAGAACTGGGTT  
16199 TTGTTTTCACACTTTAGTAGAAGAAATGTTATTACACTCAAATTTTCTAATAATTAAGGCCCAGATGGCTGTAATGTCAACAGGTC  
16290 TAGAAAAACATGAATTTTAGGAAAACATGAGTGAATCAATCAGTTGTGAATGTTTACCACACTTTTCCAGAACTGCTTGAAATATTAA  
16381 TAGTTTTGATTGTATACTGGTAGCATTCTTAAAAACCAGACTTTTAAACGGTTTATCGTTTTTTGCTTGACATACATCTAGACCTATCTA  
16472 TAAATATGGGTATGTCTATATTACATAGATACAATAAATTGACATTCATTTTAAACATTTGAAATATGACAAATTAATGTGAACTTGTA  
16563 TAATAGCTTATTATTCTATATAAGGTAGTTGCTTAATCTGTAATGTAGGTGCTTCTATTGTTGGTCATTATTTAAATAATGCCAATTAT  
16654 TAGAATAGAGAAATGAAGTTTAAAAAATTATGTTACAGGAACAATTAATGGAAGGTTTGAACCTTTTGTTCACACAATTTGAAAAATTAA  
16745 TTTCTAGCCTAATCTTGTGCTAGACATTGCTCTTAGCCTGCTGTGTTTTCTATAGGTGATAGCAGATACATAATGCTAAACATCAGGTT  
16836 TGAAATTACTGTGCTGACTTTAGTGACTGAGAAGTATCAGTCTCTTATTTGGGTAGGGGACATGGGGAATGTCATGTTTGACTTGACATCA  
16927 CAAACGATGTTTTATTGTCAGTTGCAGATACTCGCAGATACCGCAGTGGCTCGGATGAGAAACAAGAGGAGCCGGTGCCATTAAACCA  
17018 GAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAGTGGAATAGTGTCTTCTCTTGGTATGTTGGTGACATGTGTC  
17109 TGGTTGATTTTTTCAATTCATGTCTTCTGTCTTCTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGAGACAGAGTCTCACTCTGTTGCACAGGCT  
17200 GGAGTGCACTGGCGCAATCTCAGTTCACTGCAACCTCCGCCCTCCCGGTTCTTCATGCCTCAGCCTCCTGATTAGCTGGGATTACAGGCGT  
17291 GCACCACCACACCTGGCTAATTTTTTTTGTATCTTTTAGTAGAGACGGGTTTCGCCATGTTGGCCAGGCTGGTCTCAAACCTCCCAACCTC  
17382 AGATGGTACACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCACGCTCTTCTGTCTCTTCTGATGGGAGA  
17473 ACTCAGCTTAGAGCAGGCATTGATTATTTCCGCCTCATTGTTGCTGGAAGAATCATTGTGAGGCTGGCAGCTGAGGTGCACACAAGTCAGA  
17564 AAGGGTTCTGGCAACAGCAAGAGATGTGCAGATCAAATTCAGGCAGTCCAGTGGTGCTGAGTTCAAGTTCAAGAAACCGGAAAAGAGGAA  
17655 AACTTGGGAAATCTGAAATCCTTGCAAGGAGATCAAACCAAGGCTCTCTGAGGGTGGAGGCTTAGGCTGTGTTTCACTCTATGTGTGTGTA  
17746 ATTACATACAGTGAATGCCTCCAAAAAAGAGCTGAAGGAGGCTGGTAGCTTAGCGTAAGGGCTTCTTAAACAAGACTGCAGCTTTTCTA  
17837 GGACCCAGGGAGCCTAAGGAGGGTTGTTTGGCTCTGTCTTTTGCATGGACTCTGTGGGCTCAAAGAGGGGCTCCTCTGGGAATGTATCC  
17928 TCTGATTCACTTGAAGTGGGATTCACTCTGTTTCAATGATGAGCTCTGACTATCCCTTGTGAAGACAGCACTGCATCCTCAATGTCAATTT  
18019 ACTTTCACATTTCAATGTAGGGTATAGATGTGCAGAGAATTTAACTTTCTTCTCCCGTGAGAAAGCAGCATCCTGACCTAACTCTTCTTGC  
18110 TGGATGACTTCTTGTCTTCTTCTGCACTTAGCAAGCTCCATCACCATGAGGATTGGGGGACAGTGAGGCAGGAAGATGAGACAGAGA

FIG. 7  
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18201 AAAGACATTTGAGATTTGACATCACCGATCTTACTGTTGGAGAAATATGTGTGACCTCCTCCACCTTTCTAATATCCGCTTTACCAAAGT  
18292 TAGCTGCTTGAGGTGGTATATGCCCTTTTACATTATTTGCCCTCTAAGGGAAGAACTCAAAGGCCAAAGTTCACCTGTTAGAACATAGTCCT  
18383 TGTGAGGTTGTATCTCAAGATTTCTTTATTTCTTGTCAACAACTCAGAATACTAAAGTTAAAGTTGCTTTATAACCTCTATTATTTC  
18474 TCCAAACTAACATTTCCCTCCCATACCCACAAATTCCTCATTGCAATTTACCAGTACATTCACCTGGATATTAGCTACGCTGCATGAAC  
18565 CAAGGGTGCAGCCTCATTTGTTGTTGTTGTTGTTGATGAGATGAGTAACAGAGAGTGCCTCAGCACTTTAAATGAATACTTGTGGCCAAA  
18656 ATATTAAAGCAAATAGCCTGAACCCACACCCAGCCAGCCAGGCAACATAAATTATGGTTAACTTCCATTACAGAGAACTCCACAAACA  
18747 TGGATTTGATTAAATTTGCTGAGCAGTTTCATGACCTTATGTTATACTTTGCACTATGTAACAAAGAAGCTAAATCTTGAACAGCAAGCTTA  
18838 TTCATGGCACCCAGCCAGTTTCTTCTCCCTGTAAGTCTAACCTCTGCTGCCAGCAGCAAGGAGAAATACTTGGAGATCTTAGCAGCA  
18929 TGAAAGCCTCTTTGTATCACTGGGATTGCAGCAGCATGATCAAGGCCAGGGGTGATCACCAGGCCACACTGCTCTAAGACAGAGGTAC  
19020 TCAGATACGTGGCTGAAAGCCTAGCTCAAATACTGCCCCAGGTGAGCCTCTTTGCTGAGTAGCGCTACTCAAAGAACACAGCTTCCCTGC  
19111 CTAGGAAGGCAGGGCTACTGGCAATAGATCTCCAGCCTAGCAGTATGTACAGTCATGGTATTTAAGAGAACACTTTGAATTTTCTGT  
19202 TGCTTGACTGTTAAGCCTCAAATTTTCTGTTGCTTGACTTCTTCCCTGGCCTCATCCCCCAATCTGCTCCCTTCCAGCCCTATAAGCAG  
19293 TACAACATGCTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCTCTGATCATGAAAATGCTGATCAGAGCCTCATTAGGAAGT  
19384 GGATTGCTGACCTGCCATCAACGCAGCTCAACAGGATTTTAGATCTACTTTTCATCTGTGTGTTATGTTTGGAGTATAAGGTAAGTCTGGA  
19475 GTGGCACAACTTTATACAGCTCTTATCTCTCAATTGCAATTCTGTCTTCTTACTCATCCCTTTGTTTGGGCCATGGAGGCATCATTAAT  
19566 TTTTCTCATTCTGTATTCAAATCCATAACCCATTGTAGGTATAGATATGATCATTTACAGGGAAAGGATCTCTGCCCTCTGCAGAGAG  
19657 AACCCCATTTCTGTTGACAGAGTTTGGCCCATAGGATGCTCCAGAGCAGCATCTCAGTGAAGCACATGTCAAACCTAGCTGGCATCACTG  
19748 TGGAGTGTACTGTTTGGTAACTCTCCCATCAACGGAGATCTCACCAGGAGCATGCTCTCTACCTCTGTCTTGTCCAGGAAACAGA  
19839 GTTCTGACAAAGTCAGTACCCAAGTCTGCAGAGTCAAGGGATGTCAAGGCCCGGCTGGAAGAGGCTTTGCTCCGTGGGGAAGGGCCAG  
19930 AGGGGAGATGATGCGCCGCCGGGCTCCAGGTGTGTTGACTGGCCCTTCCCTGCTCTCTGTCAAGCAGTTTTTCACTGTTTGTGGGAGGA  
20021 ATGTCTCCCAACATGATTAGACACCATTTACTTTCTTGAGATATTTACGGTAGTGTGACAGACAGCGGATCTGGGAGTCTGTGTGACA  
20112 TTTGTGTTAGCCCTGTGCTGTGAGGGAAGCGCTGTTCTACAATTGTAGGAACCTGAAAACAGCACCAAATGACATCTTTTAATTA  
20203 CTCGTTGATGGTAAAGGTCACCTCTAAGATGTCAGTCATGGATGAGGTGGAAGGTGTTCCCTCAAGGCTGAGGCCTTTCTATGTGACC  
20294 TTTGGCTAGTCTATCCGGAGCATGGTCAAGAACTGAACAGTCTGCCCCCAAGATCATCTTCTCGATCATTACGGGCATATTAGAATGG  
20385 AACCACTTCCCTGAAATGGCTTCAGAGTGTCCAGTCATCAAGGATTCACCACAGGAGGAATGATCTCAAAAGGCTGAGCTTGAATAG  
20476 AATGAAATCCCAGGTACCTCAGTCTTATTCCCATGCTCAAAGTAAACAGAGTGACAGCTTATTGTATTGGAAGGACACAGTGGCAG  
20567 GGAACCTGGAGGGAGCTCATAGTTTTCAGTGGTGGTCAGGCACCTCATTTGACACCATACTTTTCATACCCAATAATTCAGTAAGCCCCC  
20658 AGAGTTTCACAGGAATCTCTGCTCATGAGAAATGTCTCTGACACTCAGAAAGGCAGAGGTTCTTCTATATTCTAGTCTATCAATCAA  
20749 AGAGCGGGCCAACTTGGACATAGGTGTGGCGACTTTGTCTCTACCAGCAACCTGCATGGACTCTAATTAGCCCGAGAAATGGTGTGAGG  
20840 CTTCTCAGTTGAGCTTGTTATGAACCTTCTGGTTATCTTGGAGGGTTTCATGCTAATCAAATTCCTATCATGCAATTTCTTAACCTCAGGGA  
20931 ACGACCGATTTCCAGGCCTAAATGAAATTTGAGATGGAAGAAAGAGCAGACATTTGGCGGCAAGCTAATGAGAAGCTAGATAAGTGAGT  
21022 CACTCGGCAACTTTCTGCTACTTTTACCTAAAGTCCAAACTATTTTCCAGGCTGCTTGTATTACTGAAACAACTGCATCCTTCCAAGG  
21113 GTTAGAAAATGAAACATCATTATCTGTGTAATACAATTCATCCAGGGACCCAGGATAATCAAAGGTATAGGGAGTTGTGGTTTCCAGCTC  
21204 TTAAAAATTTGTCACATTGATAAGCATGTAAGAAAACTAATATTTCTTTAGCAACCTCAGATGGCTTAATAAAGCAGCTGATTTTGCAG  
21295 GGAGGTAGCAGGGAATAGAGAAAGCAGGACACGGTGCTAGGACCGTATACTTTCAAATCGATATTTCTTTCTGAAATATGTACAAG  
21386 ATATACATTACAGATATATTTATGTCAGTGCTACTTAAAGTTGTTTTTAAATTTGAAAACATTCTAAATGCTCCAGAATAGAAAAATATAT  
21477 TTAAAGTTGGATTGCCATCAAATGTTTTAAATCATCTTAATGACATGGGGAAATGCTTATGACATAATGTTAAATGAACAAAGCAGG  
21568 GTAGACACTTGGTTTTCTAGTAGTGTGTGGCTCACGCCGTGAATCCAGCACTTTGGGAGGCTGAGGCCGGTGGAAACACCTGAGGTGAGTA  
21659 GTTCGAGACTAGCCTGGCCAACATGGTGAACCCCGTCTCTACAAAAAATAGAAAAATAGCTGGGCATGATGGCAGATGCTGTAATCCC  
21750 AGCTACTCAGGAGGCTGAGGAGGAAGAGTCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCAAGATCGTGCCATTGCACTCCAGCCTG  
21841 GGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAAAAGAACTCAAATCTCTGATGACATATAGTCAATGTATTTTAAAGGCT  
21932 AGAAGGAAATTTACCAAATATTAATTGCGGTTTTCTTTGGGTGCTGGGAATATCGGTAATTGATGTTTTCTCTTTTATACCTTTGCTATGT  
22023 TTCTTACAGTAGATGTGTATTATAATATATATTGTTACCAGAAAAAATATATAAGAAATGAAAGATAAAAAACCTGTTTGGATCAAA  
22114 ATCTATGCTATAGATGAATAGATATATTGACGTGATTGCTATATATGCAACAATTTAGACATATGAAAGCTAAAAGTATATATGTTTGAC  
22205 TAGATAGCACATGTTTCCGATACCGTTTAGCCACAGGTAGCCTAATGAGTCCAGGGTTTGTGAGCAAAATGTCGTAGAGCTAAAATCAC  
22296 CCCTCACACACAGTTGACAAGGTAGGATACCCCATGGGTGATGAAGCACCATCAAAGGGGTATGGGCAGACTTGATTAGCAGTGCTGT  
22387 TTTGTAAATAAATGTGAGTTAATATCTTTATTGTTACCACAAGAAATGAATCATTCTGGTTAACTTATGGGACTTTGGGAGTCACATTTAT  
22478 TTTAAACATTAAGAAATAAGTATATTTTATTATAGATGTGACTTGGAAACCCAGTTGTTGGTATCATGCCTATTGCTTTGGGTATGT  
22569 TATTCTTGCATAAATCCCTGGACTGATTTATAAAATACTTGGATCGGAGAGTCCATACATTCTACTTGGGCAATGAACAACTACAC  
22660 AAATATGATGCGGTGGGTGCTACAGAAATGCTTAGGTGGTTAGCTCATCTACTCTACTAGATTAAAGAGACCCCTAAGTAGGCCTGT

22751 TTTGCCTGGGCTGTGTAACTGGTGTGTTTGGAAAACCTTTCCCTTTTGCTTGCCAGGAGCAACACAATATTGGTCCTTACCACGCATGGCCT  
 22842 ACCGGTTTGCTCTAGGTTAGTTCTCAGCCCTGCGCTACCTGGTGGGCTGCTGGTTGTGAGAGCTAATGATTACATCTACAAATTCTCAGG  
 22933 GGCTTTGTGCTTTTTTTTTTTTTTAAAAAGGGAACCATAGTAAAAATTATACTGTTCAACCTACCTACCTGGAAAAATTTATAATTATAAT  
 23024 AATGGTGTCTTTACCCCTCTTCTGATCATTTTTTCGATTATTTTGGCTCTGTTTCTTTTAGAGCAATGATCTTCAACTTAGGCTGCACATT  
 23115 AGAATCACCTGGGGAGCTTTAAACCTGTGAGTGCCAGCTGCACCCTAGACTACTTCAATTGGAACTCCAGCAGGACCCAGAAATCAGT  
 23206 ATTTGGTAAACTTCCCAGGTGATTCTATTGCCACCAATCCATTGTTTTAAAGGAATAGATGGTAAGCTTTTCTTTTCTTTTTTTTTTCT  
 23297 TTTCTTTTTTTGAGACAAGGTCTCACTCTGTCCACCCAGGCTGGAATACAGTGGCACAATCACAGCTCACTGCAGCCTTACCCTCCTGGCCT  
 23388 CAAACAATCCTCCCACCTCAGCCTCCCAAGTAGATGGGACTACAGGTGTGTACCACCACAACCTGCTTACTTTTTGTATTTTTGTAGAGAC  
 23479 AGGGTTTCACCATGTTGCCAGGCTGGTCTAAAACTCCTGGGCTCAAGTGATCCACCTGTTTTAACCTCCCAAGTGGTGGGATTACAGGC  
 23570 ATGAGCCACTGCGCCTGGTCAGATGGTAAAGCTTTTAAAAAACCAGATTAGTGTAGTGATGGTTGCACAATATGAATGTACTTAACACTA  
 23661 CTGAAGTGTATACTTACAAATGGTTAAGATGGTAAATTTTTATGTTAGGTGTACTTTATCACAATACAAAAATTTGGGAAAAACAGATTA  
 23752 GGACACTCTAGATTTGTGCTGTCCAATACAGTAGCCATTAGCCACATGTGACTATCAATGCTTGAAATATGGCTAGTTCAAATTGAGATA  
 23843 ATAAATCAAGATAAGTGAAAAATACGCACCAGATTTTGAAGGCTTATGTGAATAAAAGAATAAAATATTTCACTAGTAATTTTTATATTG  
 23934 CTTACATGGAGACAGTATTTTTATCTTTTAGGATAAACAAAATATATAAAAATAATTTCACTTTTTCTTTACTTTTTTAATGTGGTTAC  
 24025 CACAATATATAAAATGACATATGTGGCCCCATTGTTCTACTAGACAGCATTGCTCTAAATTTAAAACTAAACTAGCAGTCAATTAATTA  
 24116 AAAAGGATGATAAGGGGCGGGCACAGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCGGAGGTAAAGTGGATCACGAGGTGAGAGA  
 24207 TCGAGACCATCTGGCTAACGCGGCGAAACCCCGTCTCTACTAAAAATACAAAAAGTAGCGGGCGCGGTGGCGGGCGCCTGTAGTCCCA  
 24298 GCTACTCGGGAGGCTGAAGCAGGAGAATGGCGTGAACCCGGGAAGTGGAGCTTGCGGTGAGCCAGATTGCGCCACTGCACCTCTGCACCTCC  
 24389 AGCCTGGGCGACAGAGGGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAGGATGATGAGGTAAATGGTAAATTTGATGTTATGTGTAC  
 24480 TTTATCACGATATAAAATTTGATGGCTCATGCCTGTGGTCCAGATACTCAGGAGGCTAAGGCAGAGCATCACTTGAGCCAGGAGTTCG  
 24571 AGGCTTCAGTGAGCTATGATAGTCCACTGCACCTAGCCTGGGTGATAGAGCAAGACCCCTGTCTCTAAGGAAAAAAAAAAAAAAAAAAGCTT  
 24662 TTAGATTTCAITTTATTTTACACATATATTATCACTTGAAAAATGAGAAAAAGTGTCAAGTGGCTTGGGACCAGAGAGCCTATCCTAAACAT  
 24753 GAAAAACAGTAAACACACAGAAGTACTTATTTTTAGTCTCAGTGGTATGTAAGCAGCTGCAGTGCCCCATTATTAGGTTAATGGGA  
 24844 CGCAAGAACAGGTAAAGTGGTAACCTGGGCCAGGACATATGAGCTGATATAATGATACCCCAACCCCATGGTAACATCTTGCTACTGAGG  
 24935 CATCTTGGTAAAGTCAATTCTTCATACCTCCCTTTCCCTTGCAACTAGATTTGGATGATGATACAAAATATCCCTTTACAGCTTCACCTAGA  
 25026 TTTTATAAGAAATGGATGGGCTAGCAAAAAAACCATTCTGATTCCTTAAAGTGAAACCTAATAGAGGAGCGAGCACCAGGCAATTTCCCAT  
 25117 TCCCTAGTGGGCAATGACCAGTAATGTCCGGCAGGATATTAGATCACTGCCCCACAGGAATACAGTCTTGTTCCTCAATGAAAAGGACG  
 25208 AAAGACCCACGCACCTTGCTGAGCAACCTCAAGGTGATCTTTGGGAAGTTAAGAGGCTGACTCTCCCTGACTTGCTCTGAAGCTCCAC  
 25299 CCTTTCTAACCAGCCGCATCACTGCCAAGTTCACATCACATCCAGTCTCACTCTCTCTCGCATGTTGCAGGGGCTTCCCTTACTCAGA  
 25390 TCTAGCAATGGTTTTCATGCGTGAATACAGCCATGGCCCTGAGGCTTTAGGCAACAATCTGAGAGGGGAGCTTAATTTGCTAGTACCACT  
 25481 AATAACTGCTTCTCTACCCATAGTGTATTTTTATAATTGTCTCATCATTATTAATAATAGTGGGGATGAGGATGACCAGGAAACCTTAC  
 25572 CTAGACAGTTGTTTCGACAAGACATGAATCACAGAAGGCACCTGCACCTGTAGTTACTCAGGGCCAGTTGCTCTGTTTTCATTTCAAGGTTG  
 25663 ACTATTTTGAGATTTCTTTACACCTTGTTGTATAGATTGCCATCATGGGAACCTGGCCAGGTTTGACATGCGCTTTAATTTGACCTCTTG  
 25754 TTGTTTCTTAGAACAAAGCCGAGTTAGATCAAGAAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCTGGATATGC  
 25845 AGGAAAAACATTATCCAGGTGAGGAAAAACACCCAATCTGATTTGTTGGCCATGAATATGTTTACTAGATAAGGACTTCTTTATGCAA  
 25936 AATTGTGAAAGACATAAATGTGATCCCATAGTACCTTTTTTAAAAAATGAAGTTGAGAAGTTTACTATTTACAACAGTGTCTACCTTATA  
 26027 AATCCAGAGATACCAACATTCTTCTGGCTTCTTTGACTTAGGGCTTACTTGGAGAGGTTAGGTGTTTGGCCAGCTGACCTCTTGGTT  
 26118 AAATCTGTGTGAGTATGTACCAAGTTTATAATATGGATGTTGGGTTTATCGTTTGTATCTAGAACAGTAGTGGTAAAGTAGAATTTTTCT  
 26209 GATGGTCAACTCCAGTTGAATGATGGTCACTGTCTGATATGGGAGCTATGATTATGACTAGGCTAGGTAAAAAGAGTGCTAAATTTGACA  
 26300 AATGATGTCTTCTTTGGACTTAAATTTGTTAAGGAAAGTCATTTGTACCATGAATTTGCCATCCCTGCTGTAGAAAAATATAGCTTTGTGA  
 26391 ACTTTGTACCATACTAATTTTATCTTCTATGTGATTATTTCCACAAATTTCCCAAGCTGTCTAGGTAATAATGAGTTTAAATACCCTGAA  
 26482 AAATGAGTTCTTACATGTTTCCATTGAGAAGTCATTATTAGAGTAGGTCCAGGATTGCTTTTAGGGCTAGAAGAAATATCGTTGAACAC  
 26573 AGTGAAATCTTAATTTCTCTAATTTTGAATTGTCTAAAATCAAAGTAATCATACAAAAATAAACACAAAAAGTATGTGATATTTTGT  
 26664 TGACTTTAATATCTTTGATAACTTAAATGCTTGGTATCACATTTACCTTATCTTTATATAGCACAAATATTAGGTGCCAAATATCTATACTA  
 26755 GCCCCCAATATATTTGAGTTTTCAAAGAAAGCTGAAACCTTTTGTATTATCTCTTGGTGTGTTAGTCTTCTGTAGGTGATAAACAAG  
 26846 CTTCTATTTAGAAACATTGCTGCCACCAAGCAGCCCTGTTGTACTGGGAAGCCACAAATGTGTTTGGCATCCCATAGGAAAGCTATGT  
 26937 CTTGTATACAAAGAAAGAACTTTCCAAAAGATGTGACCCAGGATGAGGGAGATGGGCCCTATACCTTCATTAGGAACCCAGAAATTAGGTA  
 27028 TAAATCCCAACTCATTGGAAGCATTGAAATAAAGCCATTTGGAAATAGGTCCTCAGTCCCAGGTTAATGGATGATACCCATGGTGGCT  
 27119 CACCAAACTCTTAAGACTCACCCTGGACATGGAACATCAGCATTACTGAGCTAATTGTCAGGAACATCCAGTTCAATTGGCACAGTGCAGG  
 27210 GATTCAATGATGCTGTTCTTCATTCCCCCAGGCGAGCTCGGCTCTGGACTGTAAGACAGCCTGCTGGGAGGTGTTCTGAGGGTGTGGT

27301 GAATTCCTGAACTGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCGTGCTCTCATCGCCAAGGTAAACTTGGGATGC  
 27392 TTGTTTTCTTCTCTTAATTAAGAGTAAGATTCTCATCTAGCTTCATACTTCTCTCTTCAGGTGGACCAAAAGTCACAGAGCATATTAAGT  
 27483 GGCATCACAGTAAAGGCTTAAGTCTTCTTAGGAAGAAAGCAGATGCCCTGATTCTGTGGGAAGCCACCATTGGAGAGGAAAGCAGTGGCT  
 27574 CCCATATTTGAAGTGTGGACCTAACTCTAGAAGTTTAAATGGCCATTGCTGAAGGTCTATGACATGAGAACAGAGATCAACTGAGTGAC  
 27665 TTAGCAATTTCACTCTTTCTCTGTAATACCTCTGCTGAGTGAGATTAAATCCTCTATGTGACGCCCATTAGTCTTACAAAATGTCATGCCA  
 27756 TAAATGCCAGGAAGGTCAGAAATGAATTTCTCACGGCCTGAGGAATGAGGATTATCCTGGGGTAACATGCAGATTATTTTCCCTTTATT  
 27847 TATTTATTTATTTATTTTGGAGACTGAGTCTCGCTCTATCGCCAGGCTGGAGTGAGTGATACCATTCTCAGCTCACTGCAGCCTCTGCGC  
 27938 CCTGGGCTCAAGCGATTCTCATGCCCTCAGCCTCCTGAGTATTGGGATTATAGGCGTGTGCCACCGCACCCAGCTAATTTTGTATTATTAG  
 28029 TAGAGACAGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAAGTGATCCACCTGCCTCAGCCTCCCAAAGCACTGGGAT  
 28120 TACAGGCGTGAGCCCCGTTCTGGCCTATTTTCCCTTTATTGAAGATCTCAATTGGTGCCTTCTACATGGGGTCTTTTAAATTTAAAAA  
 28211 GTAAATTTCTTCTGCTCATCTTCTCAGGACCATTCTCTTTCTTTCATCACCAGTAATTTCCAGGAACCCAAAGAACTCAGGTTTCCTT  
 28302 CCATCATAGTTGTGATTTCACCAGTGAATGCGACCTGGCTCAGAGTGCAAGTTGATAACACAGCTCTGACCCCTTTTAGCTGGACAGTTCAAT  
 28393 ATTAATCTCAAGTCTACTCCATTGCTTAAATCCATCTTCTGATTACATAGCTCATTATCTTTATGGAATAATGCATTAACTCTTCTAGG  
 28484 CTTTTGTCTTGTCAAATGGACATTTGCATATTTCAACGGTCCAGAAAGTGTATCAAAGTGCCTAATGGCCCTTTATGTCT  
 28575 CTCTAGTTTGGAGACTTACTCTTTGAAGAGGAGGTGGAACAGTGTTCGACCTATGTCAACAGTCTCTGCACCACTGCAGCAGCAGCATG  
 28666 GATGTCACCCGGAGCCAAAGCCTGTGCCACCCCTTACCTCCTCATGAGGTTTCAATTTTGGAGCCACCAGTGTAAAGAGTTCAAACCACTGAG  
 28757 TGACCTGGAATCAGTAGAGAAAAATTGATGTAAAGCATCAGCTGCGAAAAAATAAGGAAATTTGCAAGTATTGCAAGTTTACTTCTGTCC  
 28848 TGTGAGAAAGAAACAATTGAGTATGTAGATAGATAGCAGCTTCCATTTTAATTTGCATCTAAAAGTGAATTCATCAGATAAATGCAAGTGGT  
 28939 CTCTATCAGTGTGTTTCTAAAATAGACAGCCAGGGGCGAGGAACGATGGCTTTTACCTATAATCCAGCACTTTGGGAGGCCGAGGTGAGT  
 29030 GGATCATTTGAAGTCAGGAGTTCAAGACTAGCCTGGCCAGCATGGTGAATCCTGTCTCTACTATAAATACAAAAATAGCCAGATGTGTTG  
 29121 GCGCATGCCTGTAATCCAAGCTACTTTGGGAGGCTGAGCGAGGAGAATTGCTTGAACCTGGGAGGCAGATATTGCAAGTGAAGCCAGATTGCC  
 29212 CCATTTCACTCCAGCCTGGACAAACAGAGTGAGACTTCATTTCAAAAAATAATAATAATAAAATAAAATAAACCAGGTGCAGTGGCTCATGTC  
 29303 TGTAATCCTAGCACTTCGGGAGGCCAAGGCAGGCAGATCAGATGAGGCCAGGAGTCCAAAGACTAGCCTGGCCAAACATGGTGAAACCCCGT  
 29394 CTCTACAATACAAAAAATTAGCCGGGTGTGGTGGCACACACGCGCCGTAATCTTAGCTACTGGGAGGCTGAGGCACGAGAATCGCTTGAAC  
 29485 CCAGGAGGCAGAGGTTGTAGTGAGCCAAAGATTGTGCCACTGTATTCCAGCCTGAGACCTGTCTCAAAAAAAGAAAGAAAGAAAT  
 29576 GGAAGAGTATTTAGATTAAAGTTATCATCTGTGGGGGAAAAAATACAATAGACAGGTTAGAATTCAGAAGAGTGTTCCTGTTTCTAAA  
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50779 ACATATACATATGCATATACATATATATGTATGTGTATATATATGTGTGTGTGTATATATATATATATATATATATTCTTTTTTTTTT  
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59333 TTATTTTACACATGGTGGTAATTGTAAGTGTAGTTAAGAAGCAATAAAAAATAAAGGGGTGATATAGATTTCTCAGGATTCAAAGGC  
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64884 CCACAGTGGATACATTTGCTTCATGAGTGCAGGAACCATGTTCACTGCTGCATTCTTACCCCTAGCCCTGCAACAAACACACAAAAGATAC  
64975 CCAATAAATATTTGTTGATTCACTAAATGAATGAATGATGAGTAGGCCTGCTTCTAGAAGTGCCTGCCAATAAGAATGTAATGCAAGCCA  
65066 CATATATAATTTTAAAAATCTAGTAGCCATATTAAAAATAATAATAGGCCAAGTGCAGTGGCTCATACATGTAATACCAGCAGTTTGGAA  
65157 GACCAAGGTGGGAGATCACTTGAGCCCAGGAGTTTGAACACAGCCTGGGCAACATGGCTAAACCCCATCTCTACCAAAAAAGATATAAAA  
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66431 TTTTGTATACGGAGTCTCACTCTGTTGCCAGGCTGGAGTGCAATGGCACCATCTCAGCTCACTGCAACCTCCACCTCCGTGGTTCAAGCA  
66522 ATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCGTCCACCACCACGCTGACTAATTTTGTATTTTAGTAGAGATGGGGTT  
66613 TTACCATGTTGGCCAAGCTGGTCTCAAATCTGACCTCAGGTGATCCACCTGCCTCTGCCTCCCAAAGTGCTG

Putative promoter sequence of human CLASP-5

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hCLASP4	NLALFDVKNKKISADFHVDLNPPSVREMLWGSSTQLASDGSF---KGSSPESYIHGIAE	390
hCLASP5	TYPSSDIYLTVVKIEKVLQOQG-----IGDCAEPYTVIKESDG-----GKSKE-KIEKLKL	317
hCLASP3	TYP SQDVFLVIKLEKVLQOQG----IGECAEPMIFKEADA-----TKNKE-KLEKLKS	382
hCLASP2	TLSLFEDIKYNRKISADFHVDLNHF SVR QMLATTSPALMNGS-----GQSPSVLKGI LHE	381
hCLASP7	TYP SPDI FLVIKLEKVLQOQG----ISECCEPYMVLKEVD T-----AKNKE-KLEKLRL	378
hCLASP1	SVALYDLDRSRKISADFHVDLNHAAVRQMLLGASVALENGNIDTITPRQSEEPHIKGLPE	479
	. . * : * : . . : :	:
hCLASP4	SQLRYIQGGIFSVTNPHEIFLVARIEKVLOGNITHCAEPIKNSDPVKTAQKVHRTAQK	450
hCLASP5	QAESFCQR-----LGKYRMPFAWAPISLSSFFNVSTLEREVTDVD SVVG RSPVGERTLA	372
hCLASP3	QADQFCQR-----LGKYRMPFAWTAIHL MNIVSSAGSLERDSTEVEISTGERKGSWSERR	437
hCLASP2	AAMQYPKOGIFS VTC PHPDIFLVARIEKVLOGSITHCAEPMKSSDSSKVAQKVLKNAKQ	441
hCLASP7	AAEQFCTR-----LGRYRMPFAWTAVHLANIVSSAGQLDRDS D----SEGERRPAWTD RR	429
hCLASP1	EWLKF PKQAVFSVS NPHSEIVLVAKIEKVL MGNI ASGA EPIKN PDSNKYAQKILKSNRQ	539
	: : : . : :	:
hCLASP4	VCSRLGQYRMPPAWAAPRI FKDTQGS LDLDGR FSPLYKQDSSKL SSED ILKLLSEYKKPE	510
hCLASP5	QSRRLSERALSLEENG VG SNFKTS-----TLSVSSFFKQEGDR LSD ED LF KFLADYKRSS	427
hCLASP3	NSSI V GRRSLERTTSGDDACNLTSFR-PATLTVTNFYKQEGDR LSD ED LF KFLADMRRPS	496
hCLASP2	ACQRLGQYRMPPAWAARTLFKDASGNLDKNARFSAIYRQDSNKLSDNDMLKFLADMRKPE	501
hCLASP7	---RRGPQ--DRASSGD DACSFSGFR-PATLTVTNFYKQEAERLSDED LF KFLADMRRPS	483
hCLASP1	FCSKLGKYRRAFAWA VR SVFKDNQGNVDRDSRF SPLFRQESSKI STED LVKLVS DYRRAD	599
	. . : : * : : : *	:
hCLASP4	--KTKLQII PGQLNITVECVPVDLSNCITSSYVPLKPFE-KNCQNITVEVEEFVPEMTKY	567
hCLASP5	SLQR RVKSI PGLLRLE ISTAPE I INCLTP EMLPVKFPF-ENTRPHKEILEFP--TRE V	484
hCLASP3	SVLRR LRPI TAQLKIDISPAPENPHYCLTELLQVLYP-DSRVRP TREILEFP--ARDV	553
hCLASP2	K-MAKLPVILGNLDITIDNVSSDFPNYNSSYIPTKQFYETCSKTPTITEVEEFVPCIPKH	560
hCLASP7	SLLRRLRPVTAQLKIDISPAPENPHFCLSPELLHIKPYT-DPRGRPTEILEFP--AREV	540
hCLASP1	R-ISKMOTIPGSL DIAVDNVPLEHPNCVTSSFI PVKPFNMMAQTEPTVEVEEFVYDSTKY	658
	: : . * : : . . : . . : *	: *
hCLASP4	CYFFT IYKNHLYVYPLQLKYDSQKTFAKARNIAVCVEFRDSD ES DASALKCIYGKPGAGSV	627
hCLASP5	YVPH TVYRNLLYVY PQRLNFVN--KLASARNITIKIQFMCG-EDASNAMPVIFGKSSGPE	541
hCLASP3	YVENTTYRNLLYIYPQSLNFAN--RQSARNITVKVQFMYG-EDPSNAMPVIFGKSSCSE	610
hCLASP2	TQPYTIYT NHLYVYPKLYKIDSQKSF AKARNIAICIEFKDSDEEDSQPLKCIYGRPGPV	620
hCLASP7	YAPH TS YRNLLYVYP HSLNFSS--RQGSVRNLAVRVYMTG-EDPSQALPVI FGKSSCSE	597
hCLASP1	CRPYRVYKNQIYIYPKHLKYDSQKCFNKARNITVCIEFNKSD EESA KLPCIY GKPEGPL	718
	* * * : * : * : . . * : : : : . * : : : * : : .	.
hCLASP4	FTTNAYAVVSHHNQNP EFYDEIKIELPIHLHQKHLLFTFYHVSCINTKGTTKKQDTVE	687
hCLASP5	FLQEVYTA VT YHNKSPDFYE EVKIKLP AKLT VNHHLLFTFYHISCOQ-----KQ GASVE	595
hCLASP3	FSKRAYTAVVYHNRS PDFHEEIKVKLPATLTDH HHLLFTFYHVSCOQ-----KQNTLE	664
hCLASP2	FTRSAFAAVLHHHQNEFYDEIKIELPTQLHEKHLLLLTFHVSCINSSKGSTKKRDVE	680
hCLASP7	FTRRAFTPVVYHNKSPDFYE EFKLHL PACVTENHHLLFTFYHVSCOP-----RPGTAE	651
hCLASP1	FTSAAYTAVLHHSQNPDFSDEVKIELPTQLHEKHHLIFS FYHTCDINAKANAKKEALE	778
	* . : : * : * : * : * : * : : : * : : : * : : : *	:
hCLASP4	TPVGFAWVPLLKDGR II TFEQQLPVSANLPPGYLNLNDAESRRQC NV DI KWVDGAKPLLK	747
hCLASP5	TLLGYSWLPILLNERLQTGSYCLPV ALEKLPPNYSMHSAEKVPLQNP HI KWAE GHKGVFN	655
hCLASP3	TPVGYT WIPMLONGRLKTGFQCLPVSL EKPPQAYSVLSP E VP---LPGMKVWDNHKGVFN	721
hCLASP2	TQVGYSWLP LLKDGVRVTSEQHIPVSANLPSGHLGYQELGMGRHYGPEIKWVDG GKPLLK	740
hCLASP7	TPVGFTWI PLLQHGRLLTGPFCLPVSV DQPPP SYSVLTPDVA---LPGMRVWDGHKGVFS	708
hCLASP1	TSVG YAWL PLMKHDQIASQEYNIPIATSLPPNYLSFQDSASGKHGGS DIKWVDG GKPLFK	838
	* : : : * : : . : : : * : : . : : : * : : : *	:

hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLYKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLNFFQYQCKTES-----GAQALGNELVKYLYKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSEGNVEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREK-----MSQSPTSNTFIRSCKNLLNVE	887
	.. : : * : * : * : * : *	
hCLASP4	ETQVMIQFLPVIIMQLER-----VLTNMTM-----EDDVP	824
hCLASP5	RLEPLVLFLHLVLDKLFQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSKDQHG	775
hCLASP3	QLEPVVRFLHLLLDKLLLVIRPPVIAGQIVNLGQASFEAMASIINRLHKNLEGNHQHG	840
hCLASP2	EGHVMIAFLPTIILNQLER-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFAEAMAHVSVSLVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLER-----VLVQNE-----EDEIT	916
	. : : * : * : *	
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVYHYVFRLEPQORDVPKSGAPTALLDPRSYHTYGRTSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHYVFRLEPNTYPNSSSPG-PGGLGGSVHYATMARSAPASLNLNRSRSLSN	899
hCLASP2	VNVTRV-IIHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKSISS	883
hCLASP1	TTVTRV-LPDIIVAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . :	
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNCRMSYYCSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVSRIIGSKGLDRNSWVNTGGPKAAPWGSNPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLAVAPGSVDDEVSRIILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLKS-----	972
	: . .	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFFHEELALQ-----MVVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRPLTKKLFHEELALQWVVCSGSVRESALQQAFFFELMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLIKSM	899
hCLASP7	-----WVVSSSAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFFAILKSM	995
	. * .. : ***	
Cadherin Cleavage		
hCLASP4	ATYLLEENKIKLERGQRFPEPTYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVNMDKRDSEHRTFRSDFRMDITTIVNVVTSEIAALLVKPQKENEQAEMNISLAF	970
hCLASP3	VHHLYFNDKLEAERKSRFERFMDDIAALVSTIASDIVSRFQKDTM---VERLNTSLAF	1076
hCLASP2	AQHLENSKVKLIRNQRFPASYHHAETVNMMLPHITQKFGDNPEA---SKNANHS LAV	956
hCLASP7	ALHLLLGQRLDTERKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNHS LAV	999
hCLASP1	AQHLIDTNKIQLERPQRFPEPSYQNELDNLMVMSDHVIWKYKDALEE---TRRATHSVAR	1052
	. : : . * * . : : : : . . . * * *	
hCLASP4	FLKRCLTLMDRGFIFNLINDYISGFSPKDP-----KVLAEYKFEFLQTCNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVFNLIIRHYCSQLSAKLSNL---ETLISMRLFLRILCSHEHYLNLN	1027
hCLASP3	FLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLDFLRIICSHEHYVTNL	1136
hCLASP2	FIKRCFTFMDRGFVFKQINNYISCFAPGDP---KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSSNPAPALLTLRMEFTRILCSHEHYVTNL	1059
hCLASP1	FLKRCFTFMDRGCFVFMVNNYISMFSGDL---KTLCOYKFDFLQEVCOHEHFIPCL	1107
	* : : : * * : * . . . . * : : * : * : * * : * *	

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Cadherin EC motif

hCLASP4 PMAFAKPKLQR-----VQDS--NLEYSLSDEYCKHHFLVGILLRETSI 1060  
hCLASP5 FFMNADTAPTSP--CPSISSONSSSCSSSFQDQKIASMFDLTSEYRQQHFLTGLFTTELAA 1085  
hCLASP3 PCSLLTPPASPSPSVSSATSQSSGFSTNVQDQKIANMFELSVFPFQQHYLAGIVLTELAV 1196  
hCLASP2 PMPFGKGRIQR-----YQDL--QLDYSLTDEFRCRNHFLVGILLREVGT 1052  
hCLASP7 PCCPLSPPASPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQQHFLAGILLTELAL 1119  
hCLASP1 PIRSANIPDPLTP-----SES---TQELHASDMPEYSVTNEFCRKHFLIGILLREVGF 1157  
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hCLASP4 ALQDN---YEIRYTAISVIKNNLIKHAEDTRYQHKNQQAQIAQLYLPFVGLLENIORL 1116  
hCLASP5 ALDAEGEGISKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAALYLPVGIILDALP-- 1143  
hCLASP3 ILDPDAEGLFGLHKKVINMVHNLSSHSDSPRYSDPQIKARVAMLYLPLIGIMETVP-- 1254  
hCLASP2 ALQEFR---EVRLIAISVLKNNLIKHSFDDRYASRSHQARIATLYLPLFGLLIENVORI 1108  
hCLASP7 ALEPEAEGAFILHKKKAI SAVHSLLCGHDTDPRYAEATVKARVAELYLPLLSIARDTLP-- 1177  
hCLASP1 ALQEDQ---DVRHLALAVLKNLMAKHSFDDRYREPRKQQAQIASLYMPYGMILDNMERI 1213  
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hCLASP4 AGRDTLYSCA-----AMPN-S---ASRDEFPCGFTSPANRGSLSLTDKDTAYGS 1160  
hCLASP5 -----QL-----CDFTVADTRRYRTSGSD----- 1162  
hCLASP3 -----QLY-----DFTETHNQRGRPICIAITDD-- 1276  
hCLASP2 NVRDVSPFPVFNAGMTVKDESALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGIASPYTT 1167  
hCLASP7 -----RLH-----DFAEGPGQRSRLASMLDSDTE 1201  
hCLASP1 YLKDLYPFTVNTSNQGSRDDLSNNGGFQSQTAIKHANSVDTSFSKDVLSNIAAFSSIAIS 1273  
. :

hCLASP4 FQ-NGHGIKREDSRGS LIPEGATGFPDQGN TGEN-----TRQSSTRSSVSQYNRLDQYE 1213  
hCLASP5 -----EEQEGAGAINQVALAIAGNNFNLKT-----SGIVLSSLPYKQYNMLNADT 1208  
hCLASP3 -----YESEGSMISQTVAMAIAGTSVPQLTR----PGSFLLTSTSGRQHTTFSAES 1324  
hCLASP2 STPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSSSTLGNSVVRCDKLDQSE 1227  
hCLASP7 -----GEGDIAGTINPSVAMAIAGGPLAPGSR---ASISQGPPTASRAGCALSAES 1249  
hCLASP1 -----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRLDQAE 1327  
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hCLASP4 TRSLLMCYLYIVKMISED TLLTYWNKVSPQELINILILEVCLFHFYRMGKRNIARVHDA 1273  
hCLASP5 TRNLMICFLWIMKNADQSLIRKWIADLPSTQLNRILDLLFICVLCFEYKKGQSSDKVSTQ 1268  
hCLASP3 SRSLLICLLWVLKNADETVLQKWFDTLSVLQNLRLDLLYLVCVSCFEYKKGKVFERNSL 1384  
hCLASP2 IKSLLMCFLYILKSMSDDALFTYWNKASTSEIMDFFTISEVCLHQFYMGKRYIARNQEG 1287  
hCLASP7 SRTLLACVLWVLKNTEPALLQWRATDLTLPQLGRLLDLLYLCLAAFEYKKGKKAERINSL 1309  
hCLASP1 TRSLLMCFLHIMKTISYETLIAYWQRAPSPESVDFFSILDVCLQNFYRLGKRNIIRKIAA 1387  
: : \* \* : : . : : : : : : : \* \* \* :

hCLASP4 WLSKHFGIDR-----KSQTMPALNRNSGVMQARLOHLSSLESS----- 1311  
hCLASP5 VLQKSRDVKAR-----LEEALLRGE GARGEMRRRAPGNDRFPGLNEN-- 1311  
hCLASP3 TFKKSKDMRAK-----LEEAILGSIGARQEMVRRSRGQLERSPSGSAFGSQ 1430  
hCLASP2 LGPIVHDRKS-----QTLFVSRNRTGMHARLQQLGSLDNS----- 1323  
hCLASP7 TFKKSLDMKAR-----LEEAILGTIGARQEMVRRSRERSPFNGPEN----- 1350  
hCLASP1 AFKFVQSTQNNGT LKGSNPSCQTSGLLAQWMHSTSRHEGHKQHRSTLPIIRGKN----- 1442  
. : . :

hCLASP4 -----FTLNHSSTTTEADIFHQALLEGNTATEVSLTVLDTISFFTQCFTQLL 1359  
hCLASP5 --LRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAHLIILDMQENIIQASS-ALD 1368  
hCLASP3 ENLRWRKDMTHWRQNTTEKLDKSRAEIEHEALIDGNLATEANLIILDTLEIVVQTVS-VTE 1489  
hCLASP2 -----LTFNHSYGHSDADV LHQSLEANIATEVCLTALDTLSLFTLAFKNQLL 1371  
hCLASP7 --VRWRKSVTHWKQTSRDVDKTKIEMEHEALVEGNLATEASLVVLDTLEIIVQTVN-LSE 1407  
hCLASP1 --ALS NPKLLQMLDNTMTS NSNEI DIVHHVDTEANIATEGCLTILDVLSLETQTHORQLQ 1500  
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hCLASP4 NNDGHNPLMKKVFVDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFY 1419  
hCLASP5 CKDS---LLGGVLRVLVNSLNCDSQSTTYLTHCFATLRALIAKFGDLLFEEVEQCDFDLCH 1425  
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHCFAQRALVSKFPELLFEEETEQCADLCL 1546  
hCLASP2 ADLGHNPMLMKKVFVDYLCFLQKHQSETALKNVFTALRSLIYKFPSTFYEGRADMCAALCY 1431  
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPELLFEEDTELCADLCL 1464  
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVNSATALKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560  
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hCLASP4 EVLKCCTSKISSSTRNEASALLYLLMRNFEYTKRKTFLRTHLQIIIVSqliADVALSGG 1479  
hCLASP5 QVLHHCSSMDVTRSQCACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483  
hCLASP3 RLLRHCCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVMSLSLSVGTSONFNE 1604  
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKSFVRTHLQVIIISVSLIADVVGIGE 1491  
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSLSVGTTONFSE 1522  
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSqliADAG-IGG 1619  
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hCLASP4 SRFQESLFIINNFANSRPMKATAFFPAEVKDLTKRIRTVLMATAQMEHEKDPemLIDLQ 1539  
hCLASP5 EHLRRSLRTILAYSEEDTAMQMPFPTQVEELLCNLSILYDTVKMREFQEDPEMLMDLM 1543  
hCLASP3 EFLRRSLKTIITYAEEDLELRETTFPDQVQDLVFNLMILSDTVKMEHQEDPEMLIDLM 1664  
hCLASP2 TRFQOQSLIINNANSRDLIKHTSFSSDVKDLTKRIRTVLMATAQMEHEKDPemLVDLQ 1551  
hCLASP7 EHLRRSLKTIITYAEEDMGLRSTFAEQVQDLMFNLHMILTDTVKMEHQEDPEMLIDLM 1582  
hCLASP1 SRFQHS LAITN NFANGDKQMKNSNFP AEVKDLTKRIRTVLMATAQMEHEKDPemLVDLQ 1679  
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transmembrane  
hCLASP4 YSLAKSYASTPELRKTLWDSMAKIHVKNGILFSEAAMCYVHVAALVAEYIHRKK----- 1592  
hCLASP5 YRIAKSYQASPDRLRLTWLQNMAGKHTKKKCYTEAAMCLVHAAALVAEYISMLEDH----- 1598  
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHAEEAQCLVHSAALVAEYISMLEDR----- 1718  
hCLASP2 YSLAKSYASTPELRKTLWDSMAKIHVKNGILFSEAAMCYVHVTALVAEYITRKG----- 1604  
hCLASP7 YRIARGYQGPSDLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYIALLEDQ----- 1637  
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGDLSEAAMCYIHIAALIAEYIKRKG YWKVEKI 1739  
\* : \* : : \* : : : : \* : : : : \*

hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD----- 1622  
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVS EDTLSPDEGVDV 1633  
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVSDDVVS PDEEGI 1753  
hCLASP2 -----VFRQGC TAFRVITPNIDEEASMMEDVGMQD----- 1634  
hCLASP7 -----RHLPGCVSFQNISSNVLEESAISDDILSPDEEGF 1672  
hCLASP1 CTASLLSEDTHPCDNSNLLTTPSGGSMFSGWPAFLSITPNIKEEGAAKEDSGMHD----- 1795  
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ITAM  
hCLASP4 ---VHYSEEVLELLEQCVDGLWKAERYEIIISEISKLVPIYEKRREFEKLTVQVYRTIHG 1679  
hCLASP5 CAGQYFTESGLVGLLEQAELFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKLQR 1693  
hCLASP3 CSGKYFTESGLVGLLEQAASFMSAGMYEAVNEVYKLVIPILEANRDAKKLSTIHGKIQE 1813  
hCLASP2 ---VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPIYEKRR----- 1677  
hCLASP7 CSGKHFTELGLVGLLEQAAGYFTMGGLYEAVNEVYKNLIPILEAHRDYKKLAAVHGKIQE 1732  
hCLASP1 ---TPYNENILVEQLYMCGEFLWKSERYELIADVKNPIIAVFEKQRDFKKLSDLIYDIHR 1852  
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ITAM DOCK motif DOCK motif ITAM  
hCLASP4 AYTKILEVMHTKKRLLGTFFRVAFYGQSFFEEEDGKEYTYKEHKLTLGLSEISRLRVKIYG 1739  
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFFG-SKFGDLDEQEFVYKEHAITKLPEISHRLEAFYG 1750  
hCLASP3 AFSKI VHQSTGWERMFGTYFRVGFGY-IFKFGDLDEQEFVYKEHAITKLAEISHRLEGFYG 1872  
hCLASP2 -----DFFEDEDGKEYTYKEHKLTLPLSEISQRLLLKIYS 1710  
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFGY-AHFGDLDEQEFVYKESITKLAEISHRLEEFYT 1791  
hCLASP1 SYLKVAEVVNSEKRLFGRYRYRVAFYGQGFEEEDGKEYTYKEHKLTLGLSEISQRLLLKIYA 1912  
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	ITAM	ITAM	
hCLASP4	ERFGTENVKIIQDSDKVNAKELDPHYAHIQVTVVKEFYFDDKELTERKTEFERNHNISRFV		1799
hCLASP5	QCFGAEFVEVIKSDTPVDKTKLDPNKAYIQITFVEHYFDEYEMKDRVTYFEKNFNLRFRM		1810
hCLASP3	ERFGEDVVEVIKSDNPVDKCKLDPNKAYIQITFVEHYFDTYEMKDRITYFDKNYNLRFRM		1932
hCLASP2	DKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIEFFDEKELQERKTEFERSHNIRFRM		1770
hCLASP7	ERFGDDVVEIIKDSYPVDKSKLDSQKAYIQITFVEHYFDTYELKDRVTYFDRNYGLRTFL		1851
hCLASP1	DKFGADNVKIIQDSNVKNPKDLDPHYAYIQVTVTHFFEEKEIEDRKTDFEMHNNIRFV		1972
	: ** : *::*:** * : .***: *::*: * : * : * : * : * : * : *		
		ITAM	DOCK motif
hCLASP4	FEAPYTLSGKKQGCGIEEQCKRRTILTTSNSFFVVKRIPINCEQQINLKPIDGATDEIKD		1859
hCLASP5	YTFPFTLEGRPRGELHEQYRRNTVLTTMHAFPIKTRISVIOKEEFVLTPIEVAIEDMCK		1870
hCLASP3	YCTPFTLDGRAHGEHHEQFKRKTILTTSHAFPIKTRVNVVTHKEEILTPIEVAIEDMQK		1992
hCLASP2	FEMPFTQTGKRQGGVEEQCKRRTILTAHCFVVKRIPVMYQHHTLNPPIEVAIDEMSK		1830
hCLASP7	FCTPFTPDGRAHGEHHEQHKRKTLLSTDHAFPIKTRIRVCHREETVLTPEVAIEDMQK		1911
hCLASP1	FETPFTLSGKKHGGVAEQCKRRTILTTSHLFFVVKRIRIQVISQSSTLNPPIEVAIDEMSR		2032
	: ** * : * : * : * : * : * : * : * : * : * : * : * : * : *		
		Coiled-coil	
hCLASP4	KTAELQKLCSSSTDVDMIQLQLKLGQWVSVQVNAGPLAYARAFLNDSQASKYPPKKVSELK		1919
hCLASP5	KTLQLAVAINQEPDDAKMLQMVLGQSVGATVNOGPLEVAQVFLAEIPADPKLYRHHNKLK		1930
hCLASP3	KTQELAFATHQDPADPKMLQMVLGQSVGTTVNOGPLEVAQVFLSEIPSDPKLFRHHNKLK		2052
hCLASP2	KVAELRQLCSSAEVDMIKLQLKLGQSVSVQVNAGPLAYARAFLLDNTNKRYPDNKVKLLK		1890
hCLASP7	KTRELAFAEQDPPDAKMLQMVLGQSVGPTVNOGPLEVAQVFLAEIPEDPKLFRHHNKLK		1971
hCLASP1	KVSELNQLCTMEEVDMISLQLKLGQSVSVKVNAGPMAYARAFLEETNAKKYPDNQVKLLK		2092
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		Coiled-coil	
hCLASP4	DMFRKFIQACSIALELNERLIKEDQVEYHEGLKSNFRDMVKELSDDIHEQILQEDTMHSP		1979
hCLASP5	LCFKEFIMRCGRAVEKNKRLITADQREYQQLKKNYNKLKENLRPMIERKIPELYKPIFR		1990
hCLASP3	LCFKDFTKRCEPALRKNKSLIGPVQKEYQRELGLKSSP-----		2090
hCLASP2	EVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEEKTS-		1949
hCLASP7	LCFKDFCKKCEPALRKNKALIGPDQKEYHRELERNYCRLEALQPLLTQRLPOLMAPTP-		2030
hCLASP1	EIFRQFADACGQALDVNERLIKEDQLEYQEELRSHYKMDLSELSTVMNEQITGRDDLKSR		2152
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		PDZ ligand	
hCLASP4	WMSNTLHVFCIAISGTSSDRGYGSPHYAEV--	2008	
hCLASP5	VESQKRDSFHRSSFRKCETQLSQGS-----	2015	
hCLASP3	-----		
hCLASP2	VLPNSLHIFNAISGTPSTMVHGMTSSSSVV	1980	
hCLASP7	--PGLRNSLNRRASFRKADL-----	2047	
hCLASP1	GVDQCTRVISKATPALPTVSISSSAEV--	2180	